GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2002, 06:49:58 ; Search time 101.98 Seconds
(without alignments)
5698.593 Million cell updates/sec

Title: US-10-024-396-3
Perfect score: 2566
Sequence: 1 cgtcgccgtccccgtctcct.....aaatggaaaaaaaaaaaaaa 2566

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 0

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	1.2	34	3	US-09-032-894-93	Sequence 93, Appl
2	31	1.2	34	4	US-09-031-626-93	Sequence 93, Appl
c 3	30	1.2	30	4	US-09-264-693-7	Sequence 7, Appli
c 4	26	1.0	33	3	US-08-707-399E-5	Sequence 5, Appli
c 5	24	0.9	24	2	US-08-890-980-42	Sequence 42, Appl
c 6	24	0.9	24	3	US-08-890-979-42	Sequence 42, Appl
c 7	24	0.9	24	3	US-09-032-894-42	Sequence 42, Appl
c 8	24	0.9	24	4	US-09-031-626-42	Sequence 42, Appl
c 9	23	0.9	23	3	US-09-032-894-90	Sequence 90, Appl
c 10	23	0.9	23	4	US-09-031-626-90	Sequence 90, Appl
c 11	23	0.9	31	2	US-08-890-980-72	Sequence 72, Appl
12	23	0.9	31	2	US-08-890-980-74	Sequence 74, Appl
c 13	23	0.9	31	3	US-09-032-894-72	Sequence 72, Appl
14	23	0.9	31	3	US-09-032-894-74	Sequence 74, Appl
c 15	23	0.9	31	4	US-09-031-626-72	Sequence 72, Appl
16	23	0.9	31	4	US-09-031-626-74	Sequence 74, Appl
17	18	0.7	36	3	US-08-707-399E-4	Sequence 4, Appli
c 18	18	0.7	40	4	US-09-306-290-12	Sequence 12, Appl
c 19	17	0.7	20	2	US-08-890-980-71	Sequence 71, Appl
20	17	0.7	20	2	US-08-890-980-73	Sequence 73, Appl
c 21	17	0.7	20	3	US-09-032-894-71	Sequence 71, Appl
22	17	0.7	20	3	US-09-032-894-73	Sequence 73, Appl
c 23	17	0.7	20	4	US-09-031-626-71	Sequence 71, Appl
24	17	0.7	20	4	US-09-031-626-73	Sequence 73, Appl
c 25	17	0.7	47	4	US-08-928-465-1	Sequence 1, Appli
26	16	0.6	18	4	US-09-437-076-1	Sequence 1, Appli
c 27	16	0.6	22	4	US-08-928-465-4	Sequence 4, Appli
28	16	0.6	25	3	US-08-991-347-5	Sequence 5, Appli
29	16	0.6	25	4	US-08-991-184-1	Sequence 1, Appli
c 30	16	0.6	26	2	US-08-602-716A-1	Sequence 1, Appli
31	16	0.6	30	1	US-07-862-831A-15	Sequence 15, Appl
32	16	0.6	30	1	US-08-126-564A-15	Sequence 15, Appl
33	16	0.6	30	5	PCT-US94-09143-15	Sequence 15, Appl
34	16	0.6	33	1	US-08-324-243-4	Sequence 4, Appli
35	16	0.6	33	1	US-08-532-390-4	Sequence 4, Appli
36	16	0.6	33	3	US-08-717-294-4	Sequence 4, Appli
37	16	0.6	33	5	PCT-US95-11511-4	Sequence 4, Appli
c 38	16	0.6	34	1	US-08-324-243-3	Sequence 3, Appli
c 39	16	0.6	34	1	US-08-532-390-3	Sequence 3, Appli
c 40	16	0.6	34	3	US-08-717-294-3	Sequence 3, Appli
c 41	16	0.6	34	5	PCT-US95-11511-3	Sequence 3, Appli
42	16	0.6	37	4	US-09-058-969-11	Sequence 11, Appl
43	16	0.6	39	1	US-08-631-200-6	Sequence 6, Appli
44	16	0.6	39	1	US-08-829-553-6	Sequence 6, Appli
45	16	0.6	39	2	US-08-922-267A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-032-894-93
; Sequence 93, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Human
US-09-032-894-93

Query Match 1.2%; Score 31; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1085 ccttgtttctctcccatcctcacttcctcaa 1115
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Db 1 ccttgtttctctcccatcctcacttcctcaa 31

RESULT 2
US-09-031-626-93
; Sequence 93, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Human

US-09-031-626-93

Query Match 1.2%; Score 31; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1085 ccttgtttctctcccatcctcacttcctcaa 1115
||||||||||||||||||||||||||||||
Db 1 ccttgtttctctcccatcctcacttcctcaa 31

RESULT 3
US-09-264-693-7/c
; Sequence 7, Application US/09264693
; Patent No. 6261760
; GENERAL INFORMATION:
; APPLICANT: Fielding, Christopher E
; APPLICANT: Fielding, Phoebe E
; TITLE OF INVENTION: REGULATION OF THE CEL CYCLE BY STEROLS
; FILE REFERENCE: 2500.141US1 Regulation of cell cycle
; CURRENT APPLICATION NUMBER: US/09/264,693
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 60/077,351
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo
; OTHER INFORMATION: nucleotide probe to CLA-1 mRNA = nucleotides
; OTHER INFORMATION: 1514-1543 of human CLA-1 cDNA
US-09-264-693-7

Query Match 1.2%; Score 30; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 aggataaggaggccattcaggcctattctg 1543
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Db 30 AGGATAAGGAGGCCATTCAGGCCTATTCTG 1

RESULT 4
US-08-707-399E-5/c
; Sequence 5, Application US/08707399E
; Patent No. 6008014
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan and Gimeno, Carlos
; TITLE OF INVENTION: Lipid Metabolic Pathway Compositions
; TITLE OF INVENTION: and Therapeutic and Diagnostic Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,399E
; FILING DATE: September 4, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-707-399E-5

Query Match 1.0%; Score 26; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1576 gtgctgcaggaagcaaaactgtaggg 1601
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Db 33 GTGCTGCAGGAAGCAAAACTGTAGGG 8

RESULT 5
US-08-890-980-42/c
; Sequence 42, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-890-980-42

Query Match 0.9%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      67 gacatgggctgctccgccaaagcg 90
           |||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   6
US-08-890-979-42/c
; Sequence 42, Application US/08890979
; Patent No. 6030778
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Ordovas, Jose M.
;    TITLE OF INVENTION:  DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
;    TITLE OF INVENTION:  DISORDERS
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,979
;      FILING DATE:  10-JUL-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-005.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-08-890-979-42


  Query Match           0.9%;  Score 24;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           |||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   7
US-09-032-894-42/c
; Sequence 42, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
;  FILE REFERENCE: MIA-005.03
;  CURRENT APPLICATION NUMBER: US/09/032,894
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,980
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Human
US-09-032-894-42


  Query Match           0.9%;  Score 24;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           |||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   8
US-09-031-626-42/c
; Sequence 42, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  APPLICANT: Ordovas, Jose M.
;  TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
;  TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
;  FILE REFERENCE: MIA-005.04
;  CURRENT APPLICATION NUMBER: US/09/031,626
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,979
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Human
US-09-031-626-42


  Query Match           0.9%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           |||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   9
US-09-032-894-90/c
; Sequence 90, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
;  FILE REFERENCE: MIA-005.03
;  CURRENT APPLICATION NUMBER: US/09/032,894
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,980
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Human
US-09-032-894-90


  Query Match           0.9%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     123 gctactgtgcgctgtgctgggcg 145
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Db      23 GCTACTGTGCGCTGTGCTGGGCG 1


RESULT  10
US-09-031-626-90/c
; Sequence 90, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  APPLICANT: Ordovas, Jose M.
;  TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
;  TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
;  FILE REFERENCE: MIA-005.04
;  CURRENT APPLICATION NUMBER: US/09/031,626
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,979
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Human
US-09-031-626-90


  Query Match             0.9%;  Score 23;  DB 4;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    123 gctactgtgcgctgtgctgggcg 145
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Db      23 GCTACTGTGCGCTGTGCTGGGCG 1


RESULT  11
US-08-890-980-72/c
; Sequence 72, Application US/08890980
; Patent No. 5998141
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    TITLE OF INVENTION:  SR-B1 NUCLEIC ACIDS AND USES THEREFOR
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,980
;      FILING DATE:  10-JUL-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-005.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "probe"
US-08-890-980-72


  Query Match             0.9%;  Score 23;  DB 2;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
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Db      23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  12
US-08-890-980-74
; Sequence 74, Application US/08890980
; Patent No. 5998141
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    TITLE OF INVENTION:  SR-B1 NUCLEIC ACIDS AND USES THEREFOR
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,980
;      FILING DATE:  10-JUL-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-005.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "probe"
US-08-890-980-74


  Query Match             0.9%;  Score 23;  DB 2;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
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RESULT  13
US-09-032-894-72/c
; Sequence 72, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
;  FILE REFERENCE: MIA-005.03
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;  CURRENT APPLICATION NUMBER: US/09/032,894
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,980
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Human
US-09-032-894-72


  Query Match             0.9%;  Score 23;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db     23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  14
US-09-032-894-74
; Sequence 74, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
;  FILE REFERENCE: MIA-005.03
;  CURRENT APPLICATION NUMBER: US/09/032,894
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,980
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Human
US-09-032-894-74


  Query Match             0.9%;  Score 23;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      9 tcaacgccgacccggttctggca 31


RESULT  15
US-09-031-626-72/c
; Sequence 72, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  APPLICANT: Ordovas, Jose M.
;  TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
;  TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
;  FILE REFERENCE: MIA-005.04
;  CURRENT APPLICATION NUMBER: US/09/031,626
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,979
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Human
US-09-031-626-72


  Query Match             0.9%;  Score 23;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db     23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  16
US-09-031-626-74
; Sequence 74, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
;  APPLICANT: Acton, Susan L.
;  APPLICANT: Ordovas, Jose M.
;  TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
;  TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
;  FILE REFERENCE: MIA-005.04
;  CURRENT APPLICATION NUMBER: US/09/031,626
;  CURRENT FILING DATE: 1998-02-27
;  EARLIER APPLICATION NUMBER: 08/890,979
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Human
US-09-031-626-74


  Query Match             0.9%;  Score 23;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      9 tcaacgccgacccggttctggca 31


RESULT  17
US-08-707-399E-4
; Sequence 4, Application US/08707399E
; Patent No. 6008014
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan and Gimeno, Carlos
;    TITLE OF INVENTION:  Lipid Metabolic Pathway Compositions
;    TITLE OF INVENTION:  and Therapeutic and Diagnostic Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/707,399E
;      FILING DATE:  September 4, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Amy E. Mandragouras
;      REGISTRATION NUMBER:  36,207
```

```
;       REFERENCE/DOCKET NUMBER:  MNI-006
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  36 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-707-399E-4


  Query Match           0.7%;  Score 18;  DB 3;  Length 36;
  Best Local Similarity  100.0%;  Pred. No. 98;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1456 caaatccggagccaagag 1473
           ||||||||||||||||||
Db      19 CAAATCCGGAGCCAAGAG 36


RESULT  18
US-09-306-290-12/c
; Sequence 12, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
;  APPLICANT: Rovera, Giovanni
;  APPLICANT: Mukhopadhyay, Sunil
;  TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
;  TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
;  FILE REFERENCE: 09924-10
;  CURRENT APPLICATION NUMBER: US/09/306,290
;  CURRENT FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 40
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer RGP
;   OTHER INFORMATION: RR797
US-09-306-290-12


  Query Match           0.7%;  Score 18;  DB 4;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 98;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2549 atggaaaaaaaaaaaaaa 2566
           ||||||||||||||||||
Db      24 ATGGAAAAAAAAAAAAAA 7


RESULT  19
US-08-890-980-71/c
; Sequence 71, Application US/08890980
; Patent No. 5998141
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    TITLE OF INVENTION:  SR-B1 NUCLEIC ACIDS AND USES THEREFOR
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,980
;      FILING DATE:  10-JUL-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-005.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "probe"
US-08-890-980-71


  Query Match           0.7%;  Score 17;  DB 2;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db      17 TCAACGCCGACCCGGTT 1


RESULT  20
US-08-890-980-73
; Sequence 73, Application US/08890980
; Patent No. 5998141
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    TITLE OF INVENTION:  SR-B1 NUCLEIC ACIDS AND USES THEREFOR
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,980
;      FILING DATE:  10-JUL-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-005.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "probe"
```

US-08-890-980-73

Query Match 0.7%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1112 tcaacgccgacccggtt 1128
          |||||||||||||||||
Db      4 TCAACGCCGACCCGGTT 20
```

RESULT 21
US-09-032-894-71/c
; Sequence 71, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-032-894-71

Query Match 0.7%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1112 tcaacgccgacccggtt 1128
          |||||||||||||||||
Db     17 TCAACGCCGACCCGGTT 1
```

RESULT 22
US-09-032-894-73
; Sequence 73, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-032-894-73

Query Match 0.7%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1112 tcaacgccgacccggtt 1128
          |||||||||||||||||
Db      4 tcaacgccgacccggtt 20
```

RESULT 23
US-09-031-626-71/c
; Sequence 71, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-031-626-71

Query Match 0.7%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1112 tcaacgccgacccggtt 1128
          |||||||||||||||||
Db     17 TCAACGCCGACCCGGTT 1
```

RESULT 24
US-09-031-626-73
; Sequence 73, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-031-626-73

Query Match 0.7%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1112 tcaacgccgacccggtt 1128
          |||||||||||||||||
Db      4 tcaacgccgacccggtt 20
```

RESULT 25
US-08-928-465-1/c
; Sequence 1, Application US/08928465
; Patent No. 6204024
; GENERAL INFORMATION:
; APPLICANT: Romano, Joseph
; APPLICANT: Lee, Eun Mi
; TITLE OF INVENTION: CCR5 RNA Transcription Based
; TITLE OF INVENTION: Amplification Assay
; NUMBER OF SEQUENCES: 10

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Akzo No. 6204024el Patent Department
;      STREET:  1300 Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,465
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gormley, Mary E.
;      REGISTRATION NUMBER:  34,409
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-948-7400
;      TELEFAX:  301-948-9751
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  47 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA Oligonucleotide"
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..25
;      OTHER INFORMATION:  /label= T7 RNA Polymere
US-08-928-465-1


  Query Match             0.7%;  Score 17;  DB 4;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgctc 1311
          |||||||||||||||||
Db     41 TGGTCCTGCCGCTGCTC 25


RESULT  26
US-09-437-076-1
; Sequence 1, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
;  APPLICANT: Barber-Guillem, Emilio
;  APPLICANT: Nelson, M. Bud
;  APPLICANT: Castro, Stephanie
;  TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
;  CURRENT APPLICATION NUMBER: US/09/437,076
;  CURRENT FILING DATE: 1999-11-09
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE:
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Word for Windows
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   OTHER INFORMATION: synthesized
US-09-437-076-1


  Query Match             0.6%;  Score 16;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      2 ggaaaaaaaaaaaaaa 17


RESULT  27
US-08-928-465-4/c
; Sequence 4, Application US/08928465
; Patent No. 6204024
; GENERAL INFORMATION:
;    APPLICANT:  Romano, Joseph
;    APPLICANT:  Lee, Eun Mi
;    TITLE OF INVENTION:  CCR5 RNA Transcription Based
;    TITLE OF INVENTION:  Amplification Assay
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Akzo No. 6204024el Patent Department
;      STREET:  1300 Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,465
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gormley, Mary E.
;      REGISTRATION NUMBER:  34,409
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-948-7400
;      TELEFAX:  301-948-9751
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA Oligonucleotide"
;    HYPOTHETICAL:  NO
US-08-928-465-4


  Query Match             0.6%;  Score 16;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db     16 TGGTCCTGCCGCTGCT 1


RESULT  28
US-08-991-347-5
; Sequence 5, Application US/08991347
; Patent No. 6107032
; GENERAL INFORMATION:
;  APPLICANT: PBO, Svante
;  APPLICANT: KILGER, Christian
;  TITLE OF INVENTION: METHOD FOR THE DIRECT EXPONENTIAL AMPLIFICATION AND
;  TITLE OF INVENTION: SEQUENCING OF DNA MOLECULES AND ITS APPLICATION
;  FILE REFERENCE: 1614-7089
;  CURRENT APPLICATION NUMBER: US/08/991,347
```

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;  CURRENT FILING DATE: 1997-12-16
;  EARLIER APPLICATION NUMBER: DE 19653439.9
;  EARLIER FILING DATE: 1996-12-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PRIMER
US-08-991-347-5


  Query Match             0.6%;  Score 16;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 tggtcctgccgctgct 19


RESULT  29
US-08-991-184-1
; Sequence 1, Application US/08991184
; Patent No. 6225092
;  GENERAL INFORMATION:
;    APPLICANT:  P  BO, Svante
;    APPLICANT:  KILGER, Christian
;    TITLE OF INVENTION:  Method for uncoupled, direct, exponential
;    TITLE OF INVENTION:  amplification and sequencing of DNA molecules with the additic
;    TITLE OF INVENTION:  thermostable DNA polymerase and its application
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;      STREET:  655 Fifteenth Street, N.W.; Stuite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/991,184
;      FILING DATE:  16-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 196 53 494.1
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wong, King L.
;      REGISTRATION NUMBER:  37,500
;      REFERENCE/DOCKET NUMBER:  1614-7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 638-5000
;      TELEFAX:  (202) 638-4810
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
US-08-991-184-1


  Query Match             0.6%;  Score 16;  DB 4;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT  30
US-08-602-716A-1/c
; Sequence 1, Application US/08602716A
; Patent No. 5962664
;  GENERAL INFORMATION:
;    APPLICANT:  FRIEDHOFF, Arnold J.
;    APPLICANT:  BASHAM, Daryl A.
;    APPLICANT:  MILLER, Jeanette C.
;    TITLE OF INVENTION:  PSYCHOSIS PROTECTING NUCLEIC ACID,
;    TITLE OF INVENTION:  PEPTIDES, COMPOSITIONS AND METHODS OF USE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,716A
;      FILING DATE:  23-FEB-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/060,560
;      FILING DATE:  13-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05545
;      FILING DATE:  13-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  FRIEDHOFF=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-602-716A-1


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     18 GGAAAAAAAAAAAAAA 3


RESULT  31
US-07-862-831A-15
; Sequence 15, Application US/07862831A
; Patent No. 5356802
;  GENERAL INFORMATION:
;    APPLICANT:  Chandrasegaran, Srinivasan
```

```
;    TITLE OF INVENTION:  Functional Domains in FokI Restriction
;    TITLE OF INVENTION:  Endonuclease
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L St., N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/862,831A
;      FILING DATE:  19920403
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul  N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/4130/93738/SLO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-862-831A-15


  Query Match           0.6%;  Score 16;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      14 GGAAAAAAAAAAAAAA 29


RESULT  32
US-08-126-564A-15
; Sequence 15, Application US/08126564A
; Patent No. 5436150
;  GENERAL INFORMATION:
;    APPLICANT:  Chandrasegaran, Srinivasan
;    TITLE OF INVENTION:  Functional Domains in FokI
;    TITLE OF INVENTION:  Restriction Endonuclease
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1100 New York Ave., N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0,
;      SOFTWARE:  Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/126,564A
;      FILING DATE:  27-SEPTEMBER-93
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/4130/82506/CLB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3503
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-126-564A-15


  Query Match           0.6%;  Score 16;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      14 GGAAAAAAAAAAAAAA 29


RESULT  33
PCT-US94-09143-15
; Sequence 15, Application PC/TUS9409143
;  GENERAL INFORMATION:
;    APPLICANT:  Chandrasegaran, Srinivasan
;    TITLE OF INVENTION:  Functional Domains in FokI
;    TITLE OF INVENTION:  Restriction Endonuclease
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1100 New York Ave., N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0,
;      SOFTWARE:  Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09143
;      FILING DATE:  23-AUG-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/126,564
;      FILING DATE:  27-SEPTEMBER-93
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kokulis, Paul N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  PNK/4130/82506/CLB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3503
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US94-09143-15


  Query Match           0.6%;  Score 16;  DB 5;  Length 30;
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```
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     14 GGAAAAAAAAAAAAAA 29


RESULT  34
US-08-324-243-4
; Sequence 4, Application US/08324243
; Patent No. 5786464
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    TITLE OF INVENTION:  OVEREXPRESSION OF MAMMALIAN AND VIRAL
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,243
;      FILING DATE:  19-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, PAUL T
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/226001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-324-243-4


  Query Match             0.6%;  Score 16;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    225 cttcaacatgtggaag 240
          ||||||||||||||||
Db     10 CTTCAACATGTGGAAG 25


RESULT  35
US-08-532-390-4
; Sequence 4, Application US/08532390
; Patent No. 5795737
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  High Level Expression of Proteins
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/532,390
;      FILING DATE:  22-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/324,243
;      FILING DATE:  19-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LECH, KAREN F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/294001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-532-390-4


  Query Match             0.6%;  Score 16;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    225 cttcaacatgtggaag 240
          ||||||||||||||||
Db     10 CTTCAACATGTGGAAG 25


RESULT  36
US-08-717-294-4
; Sequence 4, Application US/08717294
; Patent No. 6114148
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,294
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/345001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
```

```
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-08-717-294-4


  Query Match             0.6%;  Score 16;  DB 3;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      10 CTTCAACATGTGGAAG 25


RESULT  37
PCT-US95-11511-4
; Sequence 4, Application PC/TUS9511511
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    TITLE OF INVENTION:  OVEREXPRESSION OF MAMMALIAN AND VIRAL
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11511
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, PAUL T
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/226001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-11511-4


  Query Match             0.6%;  Score 16;  DB 5;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      10 CTTCAACATGTGGAAG 25


RESULT  38
US-08-324-243-3/c
; Sequence 3, Application US/08324243
; Patent No. 5786464
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    TITLE OF INVENTION:  OVEREXPRESSION OF MAMMALIAN AND VIRAL
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,243
;      FILING DATE:  19-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, PAUL T
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/226001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-324-243-3


  Query Match             0.6%;  Score 16;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      29 CTTCAACATGTGGAAG 14


RESULT  39
US-08-532-390-3/c
; Sequence 3, Application US/08532390
; Patent No. 5795737
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  High Level Expression of Proteins
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/532,390
;      FILING DATE:  22-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/324,243
```

```
;       FILING DATE:  19-SEP-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  LECH, KAREN F.
;       REGISTRATION NUMBER:  35,238
;       REFERENCE/DOCKET NUMBER:  00786/294001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  34 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-532-390-3


  Query Match             0.6%;  Score 16;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      29 CTTCAACATGTGGAAG 14


RESULT  40
US-08-717-294-3/c
; Sequence 3, Application US/08717294
; Patent No. 6114148
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,294
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/345001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-08-717-294-3


  Query Match             0.6%;  Score 16;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      29 CTTCAACATGTGGAAG 14


RESULT  41
PCT-US95-11511-3/c
; Sequence 3, Application PC/TUS9511511
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    TITLE OF INVENTION:  OVEREXPRESSION OF MAMMALIAN AND VIRAL
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11511
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, PAUL T
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/226001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-11511-3


  Query Match             0.6%;  Score 16;  DB 5;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     225 cttcaacatgtggaag 240
           ||||||||||||||||
Db      29 CTTCAACATGTGGAAG 14


RESULT  42
US-09-058-969-11
; Sequence 11, Application US/09058969A
; Patent No. 6228603
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  APPLICANT: Deveraux, Quinn
;  APPLICANT: Salvesen, Guy S.
;  APPLICANT: Takahashi, Ryosuke
;  APPLICANT: Roy, Natalie
;  TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
;  TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation of Caspase Activity
;  FILE REFERENCE: LJ 3080
;  CURRENT APPLICATION NUMBER: US/09/058,969A
```

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;  CURRENT FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 08/862,087
;  EARLIER FILING DATE: 1997-05-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 37
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-058-969-11


  Query Match             0.6%;  Score 16;  DB 4;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    632 tgaatctcatcaacaa 647
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Db     20 tgaatctcatcaacaa 35


RESULT  43
US-08-631-200-6
; Sequence 6, Application US/08631200
; Patent No. 5646040
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/631,200
;      FILING DATE:  12-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-631-200-6


  Query Match             0.6%;  Score 16;  DB 1;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    463 gactacatcgtcatgc 478
          ||||||||||||||||
Db     15 GACTACATCGTCATGC 30


RESULT  44
US-08-829-553-6
; Sequence 6, Application US/08829553
; Patent No. 5817762
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,553
;      FILING DATE:  28-MAR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/631,200
;      FILING DATE:  12-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7853-057
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-829-553-6


  Query Match             0.6%;  Score 16;  DB 1;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    463 gactacatcgtcatgc 478
          ||||||||||||||||
Db     15 GACTACATCGTCATGC 30


RESULT  45
US-08-922-267A-6
; Sequence 6, Application US/08922267A
; Patent No. 5861239
;  GENERAL INFORMATION:
;    APPLICANT:  Kleyn, Patrick W.
;    APPLICANT:  Moore, Karen J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;    TITLE OF INVENTION:  DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
;    NUMBER OF SEQUENCES:  82
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
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;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/922,267A
;       FILING DATE:  2-SEP-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/829,553
;       FILING DATE:  28-MAR-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/631,200
;       FILING DATE:  12-APR-1996
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  7853-085
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  39 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-922-267A-6


  Query Match             0.6%;  Score 16;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     463 gactacatcgtcatgc 478
           ||||||||||||||||
Db      15 GACTACATCGTCATGC 30


Search completed: April 20, 2002, 10:09:55
Job time: 11997 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2002, 08:30:39 ; Search time 237.97 Seconds
(without alignments)
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Perfect score: 2566
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		31	1.2	34	20	AAX24560	Human SR-BI gene e
2		31	1.2	34	20	AAX24652	Human SR-BI gene e
c 3		30	1.2	30	20	AAZ21075	Human cell-surface
c 4		26	1.0	33	19	AAV11550	Human SR-BI gene P
c 5		24	0.9	24	20	AAX24511	Human SR-BI gene e
c 6		24	0.9	24	20	AAX24603	Human SR-BI gene e
c 7		23	0.9	23	20	AAX24557	Human SR-BI gene e
c 8		23	0.9	23	20	AAX24649	Human SR-BI gene e
c 9		23	0.9	31	20	AAX24543	Human SR-BI gene e
10		23	0.9	31	20	AAX24545	Human SR-BI gene e
c 11		23	0.9	31	20	AAX24635	Human SR-BI gene e
12		23	0.9	31	20	AAX24637	Human SR-BI gene e
c 13		18	0.7	21	16	AAQ75789	Reverse transcript
14		18	0.7	36	19	AAV11549	Human SR-BI gene P
c 15		18	0.7	40	22	AAH20331	Rabies virus glyco
c 16		17	0.7	17	18	AAX69803	Human fltl VEGF re
c 17		17	0.7	20	16	AAQ75604	Reverse transcript
c 18		17	0.7	20	20	AAX24542	Human SR-BI gene e
19		17	0.7	20	20	AAX24544	Human SR-BI gene e
c 20		17	0.7	20	20	AAX24634	Human SR-BI gene e
21		17	0.7	20	20	AAX24636	Human SR-BI gene e
c 22		17	0.7	21	16	AAQ75787	Reverse transcript
c 23		17	0.7	21	16	AAQ75788	Reverse transcript
c 24		17	0.7	21	16	AAQ75790	Reverse transcript
c 25		17	0.7	25	21	AAC96163	16s rRNA gene PCR
c 26		17	0.7	27	20	AAX23563	Deletion sequence
27		17	0.7	31	22	AAF86334	PCR primer 3 speci
c 28		17	0.7	47	20	AAX28398	Primer for CCR5 ge
c 29		16	0.6	17	18	AAX69802	Human fltl VEGF re
c 30		16	0.6	17	18	AAX69804	Human fltl VEGF re
c 31		16	0.6	18	19	AAV54175	Nucleotide sequenc
32		16	0.6	18	21	AAA58385	Polynucleotide # 1
c 33		16	0.6	18	21	AAZ90651	Human adipose tiss
c 34		16	0.6	19	16	AAQ75558	Reverse transcript
c 35		16	0.6	20	16	AAQ75603	Reverse transcript
c 36		16	0.6	20	16	AAQ75605	Reverse transcript
c 37		16	0.6	20	16	AAQ75606	Reverse transcript
c 38		16	0.6	20	20	AAZ31280	CCR5 gene inhibiti
c 39		16	0.6	20	21	AAZ72142	Human biallelic ma
c 40		16	0.6	21	16	AAQ75791	Reverse transcript
c 41		16	0.6	21	16	AAQ75792	Reverse transcript
c 42		16	0.6	21	16	AAQ75793	Reverse transcript
c 43		16	0.6	21	16	AAQ75794	Reverse transcript
c 44		16	0.6	21	16	AAQ75795	Reverse transcript
c 45		16	0.6	21	16	AAQ75796	Reverse transcript

ALIGNMENTS

RESULT 1
AAX24560
ID AAX24560 standard; DNA; 34 BP.
XX
AC AAX24560;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human SR-BI gene exon 8 PCR primer.
XX
KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW low density lipoprotein; LDL; high density lipoprotein; HDL;
KW diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9902735-A2.
XX
PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-US14354.
XX
PR 27-FEB-1998; 98US-0031626.
PR 10-JUL-1997; 97US-0890979.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (UYTU-) UNIV TUFTS.
XX
PI Acton SL, Ordovas JM;
XX
DR WPI; 1999-120935/10.

```
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 5; Page 72; 102pp; English.
XX
CC   A PCR primer pair (see also AAX24561) is designed for the
CC   amplification of exon 8 (see AAX24505) of the human SR-BI gene.
CC   A C/T polymorphism has been detected at nucleotide 41 of this
CC   exon.  PCR amplification followed by HaeIII digestion yields
CC   154, 33 and 31 bp products in CC individuals, 154, 64, 33 and 31
CC   bp products in CT individuals, and 154 and 64 bp products in TT
CC   individuals.  The invention is based on the discovery of the
CC   genomic structure of the human SR-BI gene (see AAX24498-509) and on
CC   the identification of polymorphic regions within the gene which are
CC   associated with abnormal body mass index (BMI) and abnormal
CC   lipoprotein levels and hence with disorders such as obesity,
CC   cachexia, cardiovascular disorders and gallstone formation.  The
CC   invention provides methods for determining whether a subject has,
CC   or is at risk of developing, a disease associated with a specific
CC   allele of a polymorphic region of an SR-BI gene.  Kits comprising
CC   the relevant probe or primer are claimed.
XX
SQ   Sequence 34 BP; 4 A; 15 C; 3 G; 12 T; 0 other;


  Query Match           1.2%;  Score 31;  DB 20;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1085 ccttgtttctctcccatcctcacttcctcaa 1115
             |||||||||||||||||||||||||||||||
Db         1 ccttgtttctctcccatcctcacttcctcaa 31


RESULT  2
AAX24652
ID   AAX24652 standard; DNA; 34 BP.
XX
AC   AAX24652;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 PCR primer.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 10; Page 71; 103pp; English.
XX
CC   A PCR primer pair (see also AAX24653) is designed for the
CC   amplification of exon 8 (see AAX24597) of the human SR-BI gene.
CC   A C/T polymorphism has been detected at nucleotide 41 of this
CC   exon.  PCR amplification followed by HaeIII digestion yields
CC   154, 33 and 31 bp products in CC individuals, 154, 64, 33 and 31
CC   bp products in CT individuals, and 154 and 64 bp products in TT
CC   individuals.  The invention is based on the discovery of the
CC   genomic structure of the human SR-BI gene (see AAX24590-601) and on
CC   the identification of polymorphic regions within the gene which are
CC   associated with abnormal body mass index (BMI) and abnormal
CC   lipoprotein levels and hence with disorders such as obesity,
CC   cachexia, cardiovascular disorders and gallstone formation.  The
CC   invention provides methods for determining whether a subject has,
CC   or is at risk of developing, a disease associated with a specific
CC   allele of a polymorphic region of an SR-BI gene.  Kits comprising
CC   the relevant probe or primer are claimed.
XX
SQ   Sequence 34 BP; 4 A; 15 C; 3 G; 12 T; 0 other;


  Query Match           1.2%;  Score 31;  DB 20;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1085 ccttgtttctctcccatcctcacttcctcaa 1115
             |||||||||||||||||||||||||||||||
Db         1 ccttgtttctctcccatcctcacttcctcaa 31


RESULT  3
AAZ21075/c
ID   AAZ21075 standard; DNA; 30 BP.
XX
AC   AAZ21075;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Human cell-surface HDL receptor CLA-1 probe.
XX
KW   LDL receptor; low density lipoprotein; steroid receptor element;
KW   caveolin; SRE; regulation; cell cycle; cholesterol; mitosis;
KW   cell division; anti-mitotic; inhibition; growth; proliferation;
KW   cancer; restenosis; atherosclerosis; heart disease; detection;
KW   lipid processing; diabetes; thyroid hormone deficiency; renal failure;
KW   inherited hyperlipidaemia; probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9946592-A1.
XX
PD   16-SEP-1999.
XX
PF   08-MAR-1999;   99WO-US05146.
XX
PR   09-MAR-1998;   98US-0077351.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Fielding CJ,  Fielding PE;
XX
DR   WPI; 1999-551504/46.
XX
PT   Detection of anti-mitotic agents for use in inhibiting the growth or
PT   proliferation of cells, e.g. in cancers or restenosis
XX
PS   Example 5; Page 92; 135pp; English.
XX
CC   A method has been developed for identifying anti-mitotic agents by
CC   detecting effects on cholesterol influx or efflux in cells or using a
```

CC caveolin promoter-reporter gene construct. The method comprises: (1)
CC contacting a cell with an agent to be tested for anti-mitotic activity;
CC and (2) detecting of the efflux of free cholesterol (FC) from the cell;
CC where an increase in efflux of FC by the cell when contacted by the
CC agent as compared to the cell under the same conditions lacking the
CC agent indicates antimitotic activity of the agent. The method can be
CC used for identifying agents for inhibiting the growth and/or
CC proliferation of cells, more particularly the growth and proliferation
CC of cancer cells, other transformed cells, or at other sites such as in
CC aortic transplant subjects to restenosis. It can also be used for
CC modulating cholesterol uptake in atherosclerosis and heart disease.
CC It can also be used for detecting lipid processing by cells in
CC pathologies such as diabetes, thyroid hormone deficiency, renal failure
CC and inherited hyperlipidaemias. The present sequence represents a
CC probe used in the exemplification of the present invention.
XX
SQ Sequence 30 BP; 7 A; 9 C; 6 G; 8 T; 0 other;

Query Match 1.2%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 aggataaggaggccattcaggcctattctg 1543
||||||||||||||||||||||||||||||
Db 30 AGGATAAGGAGGCCATTCAGGCCTATTCTG 1

RESULT 4
AAV11550/c
ID AAV11550 standard; cDNA; 33 BP.
XX
AC AAV11550;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human SR-BI gene PCR primer SRB1 3'1528r.
XX
KW Lipid metabolic pathway; h-LMP-1 gene; cardiovascular disease;
KW atherosclerosis; biliary tract disorder; gall stone; therapy;
KW diagnosis; human; SR-BI; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9809979-A1.
XX
PD 12-MAR-1998.
XX
PF 28-AUG-1997; 97WO-US15195.
XX
PR 04-SEP-1996; 96US-0707399.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton S, Gimeno CJ;
XX
DR WPI; 1998-193545/17.
XX
PT DNA encoding lipid metabolic pathway polypeptide(s) - useful for
PT treatment of cardiovascular disease or modulation of lipid uptake or
PT metabolism
XX
PS Example 1; Page 85; 102pp; English.
XX
CC PCR primer SRB1 3'1528r was used with primer SRB1 5'1387 to amplify
CC DNA encoding amino acids 463-509 (i.e. the cytoplasmic domain) of
CC human SR-BI. Restriction endonuclease EcoRI and BamHI sites were
CC engineered into the oligonucleotides to allow the cloning of the
CC SR-BI cytoplasmic domain into two-hybrid system DNA-binding domain
CC fusion vector pGBT9. This was used to identify a novel gene (see
CC AAV11547) coding for human lipid metabolic pathway (LMP) protein (see
CC AAW58888). LMP nucleic acids and polypeptides are useful for
CC developing methods for treatment of cardiovascular diseases or
CC for modulating lipid uptake or metabolism.
XX
SQ Sequence 33 BP; 6 A; 10 C; 7 G; 10 T; 0 other;

Query Match 1.0%; Score 26; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1576 gtgctgcaggaagcaaaactgtaggg 1601
||||||||||||||||||||||||||
Db 33 GTGCTGCAGGAAGCAAAACTGTAGGG 8

RESULT 5
AAX24511/c
ID AAX24511 standard; DNA; 24 BP.
XX
AC AAX24511;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human SR-BI gene exon 1 primer 3e16srb1.
XX
KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW low density lipoprotein; LDL; high density lipoprotein; HDL;
KW diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9902735-A2.
XX
PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-US14354.
XX
PR 27-FEB-1998; 98US-0031626.
PR 10-JUL-1997; 97US-0890979.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (UYTU-) UNIV TUFTS.
XX
PI Acton SL, Ordovas JM;
XX
DR WPI; 1999-120935/10.
XX
PT Detecting genetic predisposition for body mass disorders - by
PT identifying allelic variants of a polymorphic region of the SR-BI
PT gene
XX
PS Example 2; Page 67; 102pp; English.
XX
CC Primer 3e16srb1 is used with primer 5e16srb1 (see AAX24510) in the
CC PCR amplification of exon 1 (see AAX24498) of the human SR-BI gene.
CC The invention is based on the discovery of the genomic structure of
CC the human SR-BI gene (see AAX24498-509) and on the identification of
CC polymorphic regions within the gene which are associated with
CC abnormal body mass index (BMI) and abnormal lipoprotein levels and
CC hence with disorders such as obesity, cachexia, cardiovascular
CC disorders and gallstone formation. Primers (see AAX24510-35) are
CC provided for amplification of the exons, introns and promoter
CC region of the SR-BI gene for detection of polymorphisms and
CC mutations. The invention provides methods for determining whether
CC a subject has, or is at risk of developing, a disease associated
CC with a specific allele of a polymorphic region of an SR-BI gene.
CC Kits comprising the relevant probe or primer are claimed.
XX
SQ Sequence 24 BP; 3 A; 8 C; 8 G; 5 T; 0 other;

```
  Query Match             0.9%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           ||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   6
AAX24603/c
ID   AAX24603 standard; DNA; 24 BP.
XX
AC   AAX24603;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 1 primer 3e16srb1.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 10; Page 66; 103pp; English.
XX
CC   Primer 3e16srb1 is used with primer 5e16srb1 (see AAX24602) in the
CC   PCR amplification of exon 1 (see AAX24590) of the human SR-BI gene.
CC   The invention is based on the discovery of the genomic structure of
CC   the human SR-BI gene (see AAX24590-601) and on the identification of
CC   polymorphic regions within the gene which are associated with
CC   abnormal body mass index (BMI) and abnormal lipoprotein levels and
CC   hence with disorders such as obesity, cachexia, cardiovascular
CC   disorders and gallstone formation.  Claimed primers (see AAX24602-25)
CC   are used for the amplification of the exons, introns and promoter
CC   region of the SR-BI gene for detection of polymorphisms and
CC   mutations.  The invention provides methods for determining whether
CC   a subject has, or is at risk of developing, a disease associated
CC   with a specific allele of a polymorphic region of an SR-BI gene.
CC   Kits comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 24 BP; 3 A; 8 C; 8 G; 5 T; 0 other;


  Query Match             0.9%;  Score 24;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           ||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   7
AAX24557/c
ID   AAX24557 standard; DNA; 23 BP.
XX
AC   AAX24557;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 1 PCR primer.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902735-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14354.
XX
PR   27-FEB-1998;   98US-0031626.
PR   10-JUL-1997;   97US-0890979.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (UYTU-) UNIV TUFTS.
XX
PI   Acton SL,  Ordovas JM;
XX
DR   WPI; 1999-120935/10.
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 5; Page 72; 102pp; English.
XX
CC   A PCR primer pair (see also AAX24556) is designed for the
CC   amplification of exon 1 (see AAX24498) of the human SR-BI gene.
CC   A G/A polymorphism has been detected at nucleotide 146 of this
CC   exon.  PCR amplification followed by AluI digestion yields
CC   a 263 bp product in GG individuals, 263, 192 and 71 bp products
CC   in GA individuals, and 192 and 71 bp products in AA individuals.
CC   The invention is based on the discovery of the genomic structure of
CC   the human SR-BI gene (see AAX24498-509) and on the identification of
CC   polymorphic regions within the gene which are associated with
CC   abnormal body mass index (BMI) and abnormal lipoprotein levels and
CC   hence with disorders such as obesity, cachexia, cardiovascular
CC   disorders and gallstone formation.  The invention provides methods
CC   for determining whether a subject has, or is at risk of developing,
CC   a disease associated with a specific allele of a polymorphic region
CC   of an SR-BI gene.  Kits comprising the relevant probe or primer are
CC   claimed.
XX
SQ   Sequence 23 BP; 6 A; 10 C; 6 G; 1 T; 0 other;


  Query Match             0.9%;  Score 23;  DB 20;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     123 gctactgtgcgctgtgctgggcg 145
           |||||||||||||||||||||||
Db      23 GCTACTGTGCGCTGTGCTGGGCG 1
```

```
RESULT   8
AAX24649/c
ID   AAX24649 standard; DNA; 23 BP.
XX
AC   AAX24649;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 1 PCR primer.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone; PCR;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 10; Page 71; 103pp; English.
XX
CC   A PCR primer pair (see also AAX24648) is designed for the
CC   amplification of exon 1 (see AAX24590) of the human SR-BI gene.
CC   A G/A polymorphism has been detected at nucleotide 146 of this
CC   exon.  PCR amplification followed by AluI digestion yields
CC   a 263 bp product in GG individuals, 263, 192 and 71 bp products
CC   in GA individuals, and 192 and 71 bp products in AA individuals.
CC   The invention is based on the discovery of the genomic structure of
CC   the human SR-BI gene (see AAX24590-601) and on the identification of
CC   polymorphic regions within the gene which are associated with
CC   abnormal body mass index (BMI) and abnormal lipoprotein levels and
CC   hence with disorders such as obesity, cachexia, cardiovascular
CC   disorders and gallstone formation.  The invention provides methods
CC   for determining whether a subject has, or is at risk of developing,
CC   a disease associated with a specific allele of a polymorphic region
CC   of an SR-BI gene.  Kits comprising the relevant probe or primer are
CC   claimed.
XX
SQ   Sequence 23 BP; 6 A; 10 C; 6 G; 1 T; 0 other;


  Query Match             0.9%;  Score 23;  DB 20;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 3.6;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     123 gctactgtgcgctgtgctgggcg 145
           |||||||||||||||||||||||
Db      23 GCTACTGTGCGCTGTGCTGGGCG 1


RESULT   9
AAX24543/c
ID   AAX24543 standard; DNA; 31 BP.
XX
AC   AAX24543;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902735-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14354.
XX
PR   27-FEB-1998;   98US-0031626.
PR   10-JUL-1997;   97US-0890979.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (UYTU-) UNIV TUFTS.
XX
PI   Acton SL,  Ordovas JM;
XX
DR   WPI; 1999-120935/10.
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 2; Page 33; 102pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24536).
CC   It hybridises specifically to a nucleotide sequence wherein
CC   nucleotide 41 is cytidine.  The invention is based on the
CC   discovery of the genomic structure of the human SR-BI gene (see
CC   AAX24498-509) and on the identification of polymorphic regions within
CC   the gene which are associated with abnormal body mass index (BMI)
CC   and abnormal lipoprotein levels and hence with disorders such as
CC   obesity, cachexia, cardiovascular disorders and gallstone formation.
CC   The invention provides methods for determining whether a subject
CC   has, or is at risk of developing, a disease associated with a
CC   specific allele of a polymorphic region of an SR-BI gene.  Kits
CC   comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 31 BP; 7 A; 6 C; 12 G; 6 T; 0 other;


  Query Match             0.9%;  Score 23;  DB 20;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 3.5;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  10
AAX24545
ID   AAX24545 standard; DNA; 31 BP.
XX
AC   AAX24545;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
```

```
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902735-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14354.
XX
PR   27-FEB-1998;   98US-0031626.
PR   10-JUL-1997;   97US-0890979.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (UYTU-) UNIV TUFTS.
XX
PI   Acton SL,  Ordovas JM;
XX
DR   WPI; 1999-120935/10.
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 2; Page 33; 102pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24536).
CC   It hybridises specifically to the complement of a nucleotide
CC   sequence wherein nucleotide 41 is cytidine.  The invention is
CC   based on the discovery of the genomic structure of the human SR-BI
CC   gene (see AAX24498-509) and on the identification of polymorphic
CC   regions within the gene which are associated with abnormal body
CC   mass index (BMI) and abnormal lipoprotein levels and hence with
CC   disorders such as obesity, cachexia, cardiovascular disorders and
CC   gallstone formation.  The invention provides methods for
CC   determining whether a subject has, or is at risk of developing, a
CC   disease associated with a specific allele of a polymorphic region
CC   of an SR-BI gene.  Kits comprising the relevant probe or primer are
CC   claimed.
XX
SQ   Sequence 31 BP; 6 A; 12 C; 6 G; 7 T; 0 other;


  Query Match             0.9%;  Score 23;  DB 20;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db       9 tcaacgccgacccggttctggca 31


RESULT  11
AAX24635/c
ID   AAX24635 standard; DNA; 31 BP.
XX
AC   AAX24635;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 36; Page 32; 103pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24628).
CC   It hybridises specifically to a nucleotide sequence wherein
CC   nucleotide 41 of exon 8 is cytidine.  The invention is based on
CC   the discovery of the genomic structure of the human SR-BI gene (see
CC   AAX24590-601) and on the identification of polymorphic regions within
CC   the gene which are associated with abnormal body mass index (BMI)
CC   and abnormal lipoprotein levels and hence with disorders such as
CC   obesity, cachexia, cardiovascular disorders and gallstone formation.
CC   The invention provides methods for determining whether a subject
CC   has, or is at risk of developing, a disease associated with a
CC   specific allele of a polymorphic region of an SR-BI gene.  Kits
CC   comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 31 BP; 7 A; 6 C; 12 G; 6 T; 0 other;


  Query Match             0.9%;  Score 23;  DB 20;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  12
AAX24637
ID   AAX24637 standard; DNA; 31 BP.
XX
AC   AAX24637;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
```

PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-US14359.
XX
PR 27-FEB-1998; 98US-0032894.
PR 10-JUL-1997; 97US-0890980.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton SL;
XX
DR WPI; 1999-120936/10.
XX
PT New nucleic acids comprising intronic sequence of a human scavenger
PT receptor-BI (SR-B1) gene - useful for prognosis, diagnosis and
PT treatment of SR-BI associated diseases or conditions
XX
PS Claim 36; Page 32; 103pp; English.
XX
CC This probe is designed to detect a C/T polymorphism located at
CC nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24628).
CC It hybridises specifically to the complement of a sequence wherein
CC nucleotide 41 of exon 8 is cytidine. The invention is based on
CC the discovery of the genomic structure of the human SR-BI gene (see
CC AAX24590-601) and on the identification of polymorphic regions within
CC the gene which are associated with abnormal body mass index (BMI)
CC and abnormal lipoprotein levels and hence with disorders such as
CC obesity, cachexia, cardiovascular disorders and gallstone formation.
CC The invention provides methods for determining whether a subject
CC has, or is at risk of developing, a disease associated with a
CC specific allele of a polymorphic region of an SR-BI gene. Kits
CC comprising the relevant probe or primer are claimed.
XX
SQ Sequence 31 BP; 6 A; 12 C; 6 G; 7 T; 0 other;

Query Match 0.9%; Score 23; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1112 tcaacgccgacccggttctggca 1134
||||||||||||||||||||||||
Db 9 tcaacgccgacccggttctggca 31

RESULT 13
AAQ75789/c
ID AAQ75789 standard; DNA; 21 BP.
XX
AC AAQ75789;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC seperate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

Query Match 0.7%; Score 18; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2549 atggaaaaaaaaaaaaaa 2566
||||||||||||||||||
Db 21 ATGGAAAAAAAAAAAAAA 4

RESULT 14
AAV11549
ID AAV11549 standard; cDNA; 36 BP.
XX
AC AAV11549;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human SR-BI gene PCR primer SRB1 5'1387.
XX
KW Lipid metabolic pathway; h-LMP-1 gene; cardiovascular disease;
KW atherosclerosis; biliary tract disorder; gall stone; therapy;
KW diagnosis; human; SR-BI; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9809979-A1.
XX
PD 12-MAR-1998.
XX
PF 28-AUG-1997; 97WO-US15195.
XX
PR 04-SEP-1996; 96US-0707399.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton S, Gimeno CJ;
XX
DR WPI; 1998-193545/17.
XX
PT DNA encoding lipid metabolic pathway polypeptide(s) - useful for
PT treatment of cardiovascular disease or modulation of lipid uptake or
PT metabolism
XX
PS Example 1; Page 84; 102pp; English.
XX
CC PCR primer SRB1 5'1387 was used with primer SRB1 3'1528r to amplify
CC DNA encoding amino acids 463-509 (i.e. the cytoplasmic domain) of
CC human SR-BI. Restriction endonuclease EcoRI and BamHI sites were
CC engineered into the oligonucleotides to allow the cloning of the
CC SR-BI cytoplasmic domain into two-hybrid system DNA-binding domain
CC fusion vector pGBT9. This was used to identify a novel gene (see
CC AAV11547) coding for human lipid metabolic pathway (LMP) protein (see
CC AAW58888). LMP nucleic acids and polypeptides are useful for
CC developing methods for treatment of cardiovascular diseases or
CC for modulating lipid uptake or metabolism.

```
XX
SQ   Sequence 36 BP; 10 A; 9 C; 10 G; 7 T; 0 other;


  Query Match             0.7%;  Score 18;  DB 19;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1456 caaatccggagccaagag 1473
           ||||||||||||||||||
Db     19 caaatccggagccaagag 36


RESULT  15
AAH20331/c
ID   AAH20331 standard; DNA; 40 BP.
XX
AC   AAH20331;
XX
DT   01-AUG-2001  (first entry)
XX
DE   Rabies virus glycoprotein specific primer RGPRR797 SEQ ID 12.
XX
KW   Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
KW   genomic scanning; bacterial diagnostic; rabies virus glycoprotein; ss.
XX
OS   Rabies virus.
OS   Synthetic.
XX
PN   US6221635-B1.
XX
PD   24-APR-2001.
XX
PF   06-MAY-1999;   99US-0306290.
XX
PR   06-MAY-1999;   99US-0306290.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Rovera G,  Mukhopadhyay S;
XX
DR   WPI; 2001-315577/33.
XX
PT   Detecting the presence of a specific nucleic acid in a sample
PT   containing DNA, useful in scanning large genomic fragments for the
PT   presence of genes or gene families, comprises performing solid phase
PT   amplification of DNA template
XX
PS   Example 1; Column 22; 49pp; English.
XX
CC   This invention relates to a method for detecting the presence of a
CC   specific nucleic acid in a sample containing DNA. The method comprises
CC   performing solid phase amplification of DNA template (SPADT). 5' and 3'
CC   primers are irreversible bound to a solid support, and the DNA from a
CC   sample is absorbed and reversibly bound, incubated under amplification
CC   reaction conditions and the presence of the specific target DNA is
CC   detected. The method is useful for detecting the presence of a specific
CC   nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC   cell. SPADT may be used for scanning large genomic fragments for the
CC   presence of genes or gene families; or for bacterial diagnostics by
CC   examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC   for the presence of viral nucleic acid sequences in a sample. SPADT may
CC   also be used in forensic medicine by detecting and identifying species
CC   specific sequences or for the presence of major histocompatibility
CC   complex. The present sequence represents a primer specific for the rabies
CC   virus glycoprotein gene (RGP). The primer is used in an example
CC   illustrating the method of the invention.
XX
SQ   Sequence 40 BP; 6 A; 7 C; 2 G; 25 T; 0 other;


  Query Match             0.7%;  Score 18;  DB 22;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2549 atggaaaaaaaaaaaaaa 2566
           ||||||||||||||||||
Db     24 ATGGAAAAAAAAAAAAAA 7


RESULT  16
AAX69803/c
ID   AAX69803 standard; RNA; 17 BP.
XX
AC   AAX69803;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 14 U; 0 other;


  Query Match             0.7%;  Score 17;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaaa 2566
           |||||||||||||||||
Db     17 TGGAAAAAAAAAAAAAA 1


RESULT  17
AAQ75604/c
ID   AAQ75604 standard; DNA; 20 BP.
```

```
XX
AC   AAQ75604;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 16;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           |||||||||||||||||
Db      20 TGGAAAAAAAAAAAAAA 4


RESULT  18
AAX24542/c
ID   AAX24542 standard; DNA; 20 BP.
XX
AC   AAX24542;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902735-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14354.
XX
PR   27-FEB-1998;   98US-0031626.
PR   10-JUL-1997;   97US-0890979.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (UYTU-) UNIV TUFTS.
XX
PI   Acton SL,  Ordovas JM;
XX
DR   WPI; 1999-120935/10.
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 2; Page 33; 102pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24536).
CC   It hybridises specifically to a nucleotide sequence wherein
CC   nucleotide 41 is cytidine.  The invention is based on the
CC   discovery of the genomic structure of the human SR-BI gene (see
CC   AAX24498-509) and on the identification of polymorphic regions within
CC   the gene which are associated with abnormal body mass index (BMI)
CC   and abnormal lipoprotein levels and hence with disorders such as
CC   obesity, cachexia, cardiovascular disorders and gallstone formation.
CC   The invention provides methods for determining whether a subject
CC   has, or is at risk of developing, a disease associated with a
CC   specific allele of a polymorphic region of an SR-BI gene.  Kits
CC   comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db      17 TCAACGCCGACCCGGTT 1


RESULT  19
AAX24544
ID   AAX24544 standard; DNA; 20 BP.
XX
AC   AAX24544;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902735-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14354.
XX
PR   27-FEB-1998;   98US-0031626.
PR   10-JUL-1997;   97US-0890979.
XX
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PA   (MILL-) MILLENNIUM PHARM INC.
PA   (UYTU-) UNIV TUFTS.
XX
PI   Acton SL,  Ordovas JM;
XX
DR   WPI; 1999-120935/10.
XX
PT   Detecting genetic predisposition for body mass disorders - by
PT   identifying allelic variants of a polymorphic region of the SR-BI
PT   gene
XX
PS   Example 2; Page 33; 102pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24536).
CC   It hybridises specifically to the complement of a nucleotide
CC   sequence wherein nucleotide 41 is cytidine.  The invention is
CC   based on the discovery of the genomic structure of the human SR-BI
CC   gene (see AAX24498-509) and on the identification of polymorphic
CC   regions within the gene which are associated with abnormal body
CC   mass index (BMI) and abnormal lipoprotein levels and hence with
CC   disorders such as obesity, cachexia, cardiovascular disorders and
CC   gallstone formation.  The invention provides methods for
CC   determining whether a subject has, or is at risk of developing, a
CC   disease associated with a specific allele of a polymorphic region
CC   of an SR-BI gene.  Kits comprising the relevant probe or primer are
CC   claimed.
XX
SQ   Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db       4 tcaacgccgacccggtt 20


RESULT  20
AAX24634/c
ID   AAX24634 standard; DNA; 20 BP.
XX
AC   AAX24634;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 36; Page 32; 103pp; English.
XX
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24628).
CC   It hybridises specifically to a nucleotide sequence wherein
CC   nucleotide 41 of exon 8 is cytidine.  The invention is based on
CC   the discovery of the genomic structure of the human SR-BI gene (see
CC   AAX24590-601) and on the identification of polymorphic regions within
CC   the gene which are associated with abnormal body mass index (BMI)
CC   and abnormal lipoprotein levels and hence with disorders such as
CC   obesity, cachexia, cardiovascular disorders and gallstone formation.
CC   The invention provides methods for determining whether a subject
CC   has, or is at risk of developing, a disease associated with a
CC   specific allele of a polymorphic region of an SR-BI gene.  Kits
CC   comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db      17 TCAACGCCGACCCGGTT 1


RESULT  21
AAX24636
ID   AAX24636 standard; DNA; 20 BP.
XX
AC   AAX24636;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human SR-BI gene exon 8 probe.
XX
KW   SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
KW   restenosis; congestive heart failure; atherosclerosis; cholesterol;
KW   low density lipoprotein; LDL; high density lipoprotein; HDL;
KW   diagnosis; body mass index; obesity; cachexia; gallstone;
KW   probe; hybridisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902736-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US14359.
XX
PR   27-FEB-1998;   98US-0032894.
PR   10-JUL-1997;   97US-0890980.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL;
XX
DR   WPI; 1999-120936/10.
XX
PT   New nucleic acids comprising intronic sequence of a human scavenger
PT   receptor-BI (SR-B1) gene  - useful for prognosis, diagnosis and
PT   treatment of SR-BI associated diseases or conditions
XX
PS   Claim 36; Page 32; 103pp; English.
XX
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```
CC   This probe is designed to detect a C/T polymorphism located at
CC   nucleotide 41 of exon 8 of the human SR-BI gene (see AAX24628).
CC   It hybridises specifically to the complement of a sequence wherein
CC   nucleotide 41 of exon 8 is cytidine.  The invention is based on
CC   the discovery of the genomic structure of the human SR-BI gene (see
CC   AAX24590-601) and on the identification of polymorphic regions within
CC   the gene which are associated with abnormal body mass index (BMI)
CC   and abnormal lipoprotein levels and hence with disorders such as
CC   obesity, cachexia, cardiovascular disorders and gallstone formation.
CC   The invention provides methods for determining whether a subject
CC   has, or is at risk of developing, a disease associated with a
CC   specific allele of a polymorphic region of an SR-BI gene.  Kits
CC   comprising the relevant probe or primer are claimed.
XX
SQ   Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db       4 tcaacgccgacccggtt 20


RESULT  22
AAQ75787/c
ID   AAQ75787 standard; DNA; 21 BP.
XX
AC   AAQ75787;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           |||||||||||||||||
Db      20 TGGAAAAAAAAAAAAAA 4


RESULT  23
AAQ75788/c
ID   AAQ75788 standard; DNA; 21 BP.
XX
AC   AAQ75788;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           |||||||||||||||||
Db      20 TGGAAAAAAAAAAAAAA 4


RESULT  24
AAQ75790/c
ID   AAQ75790 standard; DNA; 21 BP.
XX
AC   AAQ75790;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
```

```
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           |||||||||||||||||
Db      20 TGGAAAAAAAAAAAAAA 4


RESULT  25
AAC96163/c
ID   AAC96163 standard; DNA; 25 BP.
XX
AC   AAC96163;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #130.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP03636.
XX
PR   26-APR-1999;   99EP-0303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences
PT   of specific length -
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular.
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 21;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2549 atggaaaaaaaaaaaaa 2565
           |||||||||||||||||
Db      17 ATGGAAAAAAAAAAAAA 1


RESULT  26
AAX23563/c
ID   AAX23563 standard; DNA; 27 BP.
XX
AC   AAX23563;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 16.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US18084.
XX
PR   02-SEP-1997;   97US-0923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target
PT   deletion oligonucleotides
XX
PS   Example 1; Page 94; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe
CC   oligonucleotide, which is the reverse complement of part of a unique
CC   target oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
```

```
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence
CC   for its reverse complement is not modified, the method may be performed
CC   using oligodeoxynucleotides.
XX
SQ   Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     18 TGGAAAAAAAAAAAAAA 2


RESULT  27
AAF86334
ID   AAF86334 standard; DNA; 31 BP.
XX
AC   AAF86334;
XX
DT   17-JUL-2001  (first entry)
XX
DE   PCR primer 3 specific for human ZFP-52 cDNA.
XX
KW   Human; zinc finger protein 52; ZFP-52; proliferation disorder; neoplasm;
KW   immune system disorder; metabolic disorder; cancer; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200127151-A1.
XX
PD   19-APR-2001.
XX
PF   08-OCT-2000; 2000WO-CN00308.
XX
PR   10-OCT-1999;   99CN-0116949.
XX
PA   (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-281977/29.
XX
PT   Human zinc finger protein 52 applicable in diagnosis and treatment of
PT   proliferation disorders, disorders induced by immune system, metabolic
PT   disorders, neoplasms and cancers
XX
PS   Example 5; Page 14; 30pp; Chinese.
XX
CC   This invention relates to human zinc finger protein 52 (ZFP-52) which is
CC   a member of the kruppel family of proteins. This sequence represents a
CC   PCR primer used to amplify cDNA encoding human ZFP-52. ZFP-52 protein and
CC   polynucleotide sequences can be used in the diagnosis and treatment of
CC   proliferation disorders, immune system related disorders, metabolic
CC   disorders, neoplasms and cancer.
XX
SQ   Sequence 31 BP; 16 A; 5 C; 6 G; 4 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 22;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2549 atggaaaaaaaaaaaaa 2565
           |||||||||||||||||
Db     10 atggaaaaaaaaaaaaa 26


RESULT  28
AAX28398/c
ID   AAX28398 standard; DNA; 47 BP.
XX
AC   AAX28398;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Primer for CCR5 gene.
XX
KW   Primer; CCR5 gene; non-syncytia-inducing; HIV-1; mutation detection;
KW   chemokine receptor gene; infection; disease progression prediction; ss.
XX
OS   Synthetic.
XX
PN   WO9913112-A1.
XX
PD   18-MAR-1999.
XX
PF   14-SEP-1998;   98WO-US19007.
XX
PR   12-SEP-1997;   97US-0928465.
XX
PA   (ALKU ) AKZO NOBEL NV.
XX
PI   Lee EM,  Romano JW;
XX
DR   WPI; 1999-263372/22.
XX
PT   Determination of zygosity of CCR5 chemokine receptor gene in an
PT   individual
XX
PS   Claim 6; Page 23; 36pp; English.
XX
CC   This sequence represents a primer for a region of the CCR5 gene.
CC   The invention relates to a method for the determination of susceptibility
CC   of an individual to non-syncytia-inducing (NSI) forms of human
CC   immunodeficiency virus type 1 (HIV-1), by detecting whether the
CC   individual is homozygous mutant, heterozygous or homozygous wild type for
CC   the CCR5 chemokine receptor gene. The method can be used to predict
CC   susceptibility of an individual to infection by NSI forms of HIV-1 and
CC   for predicting disease progression.
XX
SQ   Sequence 47 BP; 15 A; 14 C; 11 G; 7 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 20;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgctc 1311
           |||||||||||||||||
Db     41 TGGTCCTGCCGCTGCTC 25


RESULT  29
AAX69802/c
ID   AAX69802 standard; RNA; 17 BP.
XX
AC   AAX69802;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
```

```
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 15 U; 0 other;


  Query Match             0.6%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     17 GGAAAAAAAAAAAAAA 2


RESULT  30
AAX69804/c
ID   AAX69804 standard; RNA; 17 BP.
XX
AC   AAX69804;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW   flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US17480.
XX
PR   11-JAN-1996;   96US-0584040.
PR   26-OCT-1995;   95US-0005974.
XX
PA   (CHIR ) CHIRON CORP.
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Escobedo J,  McSwiggen J,  Pavco P,  Stinchcomb D;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT   mRNA stability  - useful for treating e.g. tumour angiogenesis,
PT   psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC   be treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention.
XX
SQ   Sequence 17 BP; 2 A; 2 C; 0 G; 13 U; 0 other;


  Query Match             0.6%;  Score 16;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
           ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  31
AAV54175/c
ID   AAV54175 standard; cDNA; 18 BP.
XX
AC   AAV54175;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 12.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP00905.
XX
PR   05-MAR-1997;   97JP-0050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis,
PT   preventing or treating diseases associated with apoptosis
XX
PS   Example 1; Page 51; 70pp; Japanese.
XX
```

```
CC   This is the nucleotide sequence of a PCR primer used in the method
CC   of the invention, involving the use of novel apoptosis-related DNAs
CC   and proteins.  The inventions can be used as diagnostic reagents for
CC   apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC   in immunohistological staining, as apoptosis inhibitors.  It can also
CC   be used for treatment of apoptosis-related diseases.
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      18 GGAAAAAAAAAAAAAA 3


RESULT  32
AAA58385
ID   AAA58385 standard; DNA; 18 BP.
XX
AC   AAA58385;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 1 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US26612.
XX
PR   10-NOV-1998;   98US-0107828.
PR   09-NOV-1999;   99US-0437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal -
XX
PS   Example 3; Page 68; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC   proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC   attached to their surfaces with one end of the polynucleotide extending
CC   outwardly from the nanocrystal. The present sequence is one such
CC   polynucleotide. These nanocrystals are used with a second series of
CC   nanocrystals, which have polynucleotides complementary to the first
CC   polynucleotides, so that the respective complementary strands hybridise
CC   to each other and form a dendrimer. This dendrimer produces a signal
CC   which can then be detected e.g. fluorescence. The present sequence is
CC   composed mainly of Adenine bases. This sequence may therefore be
CC   used with a polynucleotide composed mainly of Thymine bases (AAA58386).
XX
SQ   Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 21;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      2 ggaaaaaaaaaaaaaa 17


RESULT  33
AAZ90651/c
ID   AAZ90651 standard; DNA; 18 BP.
XX
AC   AAZ90651;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #12.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-0225228.
XX
PR   23-JUL-1998;   98JP-0225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal
PT   tissue -
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension,
CC   arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC   (AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic
CC   diagnosis, prevention and treatment of adipose tissue related diseases.
CC   Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC   tissue genes.
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 21;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      18 GGAAAAAAAAAAAAAA 3


RESULT  34
AAQ75558/c
ID   AAQ75558 standard; DNA; 19 BP.
XX
AC   AAQ75558;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
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```
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     19 GGAAAAAAAAAAAAAA 4


RESULT  35
AAQ75603/c
ID   AAQ75603 standard; DNA; 20 BP.
XX
AC   AAQ75603;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     19 GGAAAAAAAAAAAAAA 4


RESULT  36
AAQ75605/c
ID   AAQ75605 standard; DNA; 20 BP.
XX
AC   AAQ75605;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     19 GGAAAAAAAAAAAAAA 4
```

RESULT 37
AAQ75606/c
ID AAQ75606 standard; DNA; 20 BP.
XX
AC AAQ75606;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC seperate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 other;

Query Match 0.6%; Score 16; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2551 ggaaaaaaaaaaaaaa 2566
||||||||||||||||
Db 19 GGAAAAAAAAAAAAAA 4

RESULT 38
AAZ31280/c
ID AAZ31280 standard; DNA; 20 BP.
XX
AC AAZ31280;
XX
DT 24-JAN-2000 (first entry)
XX
DE CCR5 gene inhibiting antisense oligo AS(s)-37.
XX
KW HIV cofactor inhibitor; HIV infection; CXCR4 gene; CCR5 gene;
KW drug composition; antisense; ss.
XX
OS Synthetic.
XX
PN WO9951751-A1.
XX
PD 14-OCT-1999.
XX
PF 01-APR-1999; 99WO-JP01722.
XX
PR 02-APR-1998; 98JP-0125452.
XX
PA (MARI-) MARINE BIO CO LTD.
XX
PI Takaku H, Yamamoto N, Kimura T, Takai K, Wada A;
XX
DR WPI; 1999-620207/53.
XX
PT Antisense oligonucleotide-based HIV cofactor inhibitors, as drug
PT compositions for treatment of HIV infection -
XX
PS Claim 6; Page 16; 59pp; Japanese.
XX
CC The invention provides HIV cofactor inhibitors that contain
CC oligonucleotides with a base sequence complementary to the CXCR4 or CCR5
CC genes. Such inhibitors can be formulated into drug compositions for
CC prevention or treatment of HIV infection, with inhibition of expression
CC of CXCR4 or/and CCR5 gene. Sequences AAZ31244-306 represent antisense
CC oligonucleotides to the CCR5 gene.
XX
SQ Sequence 20 BP; 5 A; 8 C; 7 G; 0 U; 0 other;

Query Match 0.6%; Score 16; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1295 tggtcctgccgctgct 1310
||||||||||||||||
Db 16 TGGTCCTGCCGCTGCT 1

RESULT 39
AAZ72142/c
ID AAZ72142 standard; DNA; 20 BP.
XX
AC AAZ72142;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6498.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 9; Page 1616; 2745pp; English.

```
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 other;

  Query Match             0.6%;  Score 16;  DB 21;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1710 cacagcctgagcctcc 1725
           ||||||||||||||||
Db     20 CACAGCCTGAGCCTCC 5


RESULT 40
AAQ75791/c
ID   AAQ75791 standard; DNA; 21 BP.
XX
AC   AAQ75791;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

  Query Match             0.6%;  Score 16;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     19 GGAAAAAAAAAAAAAA 4


RESULT 41
AAQ75792/c
ID   AAQ75792 standard; DNA; 21 BP.
XX
AC   AAQ75792;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

  Query Match             0.6%;  Score 16;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     19 GGAAAAAAAAAAAAAA 4


RESULT 42
AAQ75793/c
ID   AAQ75793 standard; DNA; 21 BP.
XX
AC   AAQ75793;
XX
DT   04-AUG-1995  (first entry)
XX
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```
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      19 GGAAAAAAAAAAAAAA 4


RESULT  43
AAQ75794/c
ID   AAQ75794 standard; DNA; 21 BP.
XX
AC   AAQ75794;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      19 GGAAAAAAAAAAAAAA 4


RESULT  44
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ID   AAQ75795 standard; DNA; 21 BP.
XX
AC   AAQ75795;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-0112515.
XX
PR   16-APR-1993;   93JP-0112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA
PT   followed by digestion with restriction enzymes
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an
CC   aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC   and a plural type of labelled reverse transcription primers
CC   (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC   template for each reverse transcription primer; (b) digesting each of
CC   the prepared aggregates of the double-stranded cDNAs with restriction
CC   enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC   seperate lanes. The method can be used to analyse gene expression
CC   rapidly and easily.
XX
SQ   Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 16;  Length 21;
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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      19 GGAAAAAAAAAAAAAA 4
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RESULT 45
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ID AAQ75796 standard; DNA; 21 BP.
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AC AAQ75796;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC seperate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;

Query Match 0.6%; Score 16; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      19 GGAAAAAAAAAAAAAA 4
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Search completed: April 20, 2002, 10:14:07
Job time: 6208 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2002, 06:42:18 ; Search time 2150.98 Seconds
(without alignments)
12819.119 Million cell updates/sec

Title: US-10-024-396-3
Perfect score: 2566
Sequence: 1 cgtcgccgtccccgtctcct.....aaatggaaaaaaaaaaaaaa 2566

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 80718

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		34	1.3	40	11	R71941	R71941 yj84a06.r1
2		19	0.7	19	13	AZ962226	AZ962226 2M0231A02
c 3		19	0.7	48	13	AZ477776	AZ477776 1M0297L24
4		17	0.7	20	13	AZ818055	AZ818055 2M0087B23
c 5		17	0.7	31	11	N25903	N25903 yw79e11.s1
c 6		17	0.7	37	2	HSM002040	A1037709 Homo sapi
7		17	0.7	37	11	BG175511	BG175511 602334778
c 8		17	0.7	39	10	AW248768	AW248768 2820919.3
c 9		17	0.7	44	2	HSM009691	A1044841 Homo sapi
c 10		17	0.7	45	2	HSM003634	A1039158 Homo sapi
11		17	0.7	49	11	BF017790	BF017790 ux75h05.y
c 12		17	0.7	50	2	HSM003660	A1039184 Homo sapi
13		16	0.6	19	13	AZ853220	AZ853220 2M0156J15
c 14		16	0.6	19	13	AZ856873	AZ856873 2M0161O19
15		16	0.6	19	13	AZ950028	AZ950028 2M0213L19
c 16		16	0.6	20	13	AZ370699	AZ370699 1M0121N17
17		16	0.6	20	13	AZ406839	AZ406839 1M0176C16
c 18		16	0.6	21	13	AZ785791	AZ785791 1M0030O19
19		16	0.6	22	2	HSM002940	A1038464 Homo sapi
c 20		16	0.6	22	13	AZ309907	AZ309907 1M0017N14
c 21		16	0.6	22	13	TA386H07Q	AL498291 T. brucei
22		16	0.6	23	13	AZ390689	AZ390689 1M0152A18
23		16	0.6	24	13	AZ812579	AZ812579 2M0079A23
24		16	0.6	25	2	HSM001398	A1037073 Homo sapi
c 25		16	0.6	25	2	HSM003169	A1038693 Homo sapi
26		16	0.6	25	2	HSM003450	A1038974 Homo sapi
c 27		16	0.6	25	13	AZ832800	AZ832800 2M0113M21
c 28		16	0.6	25	13	AZ837511	AZ837511 2M0132N17
c 29		16	0.6	25	13	TA324F07P	AL493403 T. brucei
30		16	0.6	26	2	HSM001401	A1037076 Homo sapi
31		16	0.6	26	2	HSM001421	A1037096 Homo sapi
32		16	0.6	26	2	HSM002179	A1037846 Homo sapi
c 33		16	0.6	26	2	HSM002201	A1037868 Homo sapi
34		16	0.6	26	2	HSM003490	A1039014 Homo sapi
35		16	0.6	26	2	HSM003529	A1039053 Homo sapi
36		16	0.6	26	2	HSM003586	A1039110 Homo sapi
c 37		16	0.6	27	2	HSM001542	A1037217 Homo sapi
38		16	0.6	27	2	HSM002015	A1037684 Homo sapi
39		16	0.6	27	2	HSM002125	A1037793 Homo sapi
c 40		16	0.6	27	2	HSM002148	A1037815 Homo sapi
c 41		16	0.6	27	2	HSM003588	A1039112 Homo sapi
42		16	0.6	27	2	HSM003597	A1039121 Homo sapi
43		16	0.6	27	10	AV741507	AV741507 AV741507
c 44		16	0.6	27	11	N29432	N29432 yw86h10.s1
c 45		16	0.6	27	11	R31539	R31539 yh72e05.s1

ALIGNMENTS

RESULT 1
R71941
LOCUS R71941 40 bp mRNA EST 02-JUN-1995
DEFINITION yj84a06.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155410 5' similar to SP:A48528 S36656; MEMBRANE GLYCOPROTEIN CLA-1 PROTEIN LONG FORM PRECURSOR - ;, mRNA sequence.
ACCESSION R71941
VERSION R71941.1 GI:845973
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2714
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2714 Std Error: 0.00

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          Seq primer: M13RP1
          High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="GDB:573028"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155410"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT       9 a      9 c     12 g      9 t      1 others
ORIGIN


  Query Match             1.3%;  Score 34;  DB 11;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     927 gtacaaggagtcaggggtgtttgaaggcatcccc 960
           ||||||||||||||||||||||||||||||||||
Db       1 GTACAAGGAGTCAGGGGTGTTTGAAGGCATCCCC 34


RESULT 2
AZ962226
LOCUS       AZ962226       19 bp    DNA             GSS       27-APR-2001
DEFINITION  2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0231A02 F, DNA sequence.
ACCESSION   AZ962226
VERSION     AZ962226.1  GI:13833453
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0231  row: A  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0231A02"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      16 a      0 c      2 g      1 t
ORIGIN


  Query Match             0.7%;  Score 19;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2544 aaaaaatggaaaaaaaaaa 2562
           ||||||||||||||||||||
Db       1 AAAAAATGGAAAAAAAAAA 19


RESULT 3
AZ477776/c
LOCUS       AZ477776       48 bp    DNA             GSS       04-OCT-2000
DEFINITION  1M0297L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0297L24 F, DNA sequence.
ACCESSION   AZ477776
VERSION     AZ477776.1  GI:10636030
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0297  row: L  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="UUGC1M0297L24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 2 a 12 c 3 g 31 t
ORIGIN

Query Match 0.7%; Score 19; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2547 aaatggaaaaaaaaaaaaa 2565
: ||||||||||||||||||||
Db 48 AAATGGAAAAAAAAAAAAA 30

RESULT 4
AZ818055
LOCUS AZ818055 20 bp DNA GSS 20-FEB-2001
DEFINITION 2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0087B23 R, DNA sequence.
ACCESSION AZ818055
VERSION AZ818055.1 GI:12987963
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087B23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 17 a 0 c 2 g 1 t
ORIGIN

Query Match 0.7%; Score 17; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2550 tggaaaaaaaaaaaaaa 2566
||||||||||||||||
Db 1 TGGAAAAAAAAAAAAAA 17

RESULT 5
N25903/c
LOCUS N25903 31 bp mRNA EST 29-DEC-1995
DEFINITION yw79e11.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258476 3' similar to gb:X53463 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (HUMAN);, mRNA sequence.
ACCESSION N25903
VERSION N25903.1 GI:1140251
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 26
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 26.
FEATURES Location/Qualifiers
source 1. .31
/organism="Homo sapiens"

```
                     /db_xref="GDB:3888086"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:258476"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT        6 a      5 c      0 g     20 t
ORIGIN


  Query Match           0.7%;  Score 17;  DB 11;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      22 TGGAAAAAAAAAAAAAA 6


RESULT   6
HSM002040/c
ID   HSM002040  standard; RNA; EST; 37 BP.
XX
AC   AL037709;
XX
SV   AL037709.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564A157_s1  (from clone DKFZp564A157)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-37
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No r1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .37
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564A157"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   X1-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 37 BP; 4 A; 10 C; 0 G; 23 T; 0 other;


  Query Match           0.7%;  Score 17;  DB 2;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 3.3e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      22 TGGAAAAAAAAAAAAAA 6


RESULT   7
BG175511
LOCUS       BG175511       37 bp    mRNA            EST       06-FEB-2001
DEFINITION  602334778F2 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457995 5',
            mRNA sequence.
ACCESSION   BG175511
VERSION     BG175511.1  GI:12682214
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10255  row: k  column: 20
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4457995"
                     /clone_lib="NCI_CGAP_Mam1"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="3 months, virgin"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT       23 a      2 c      5 g      7 t
ORIGIN


  Query Match           0.7%;  Score 17;  DB 11;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 3.3e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       9 TGGAAAAAAAAAAAAAA 25


RESULT   8
AW248768/c
LOCUS       AW248768       39 bp    mRNA            EST       07-JAN-2000
DEFINITION  2820919.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820919 3',
            mRNA sequence.
ACCESSION   AW248768
VERSION     AW248768.1  GI:6591761
```

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820919.5prime.
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 39 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM5  row: H  column: 8
            High quality sequence stop: 7.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820919"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).".
BASE COUNT        6 a      2 c      1 g     30 t
ORIGIN


  Query Match             0.7%;  Score 17;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||||
Db      34 TGGAAAAAAAAAAAAAA 18


RESULT   9
HSM009691/c
ID   HSM009691  standard; RNA; EST; 44 BP.
XX
AC   AL044841;
XX
SV   AL044841.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434B083_s1  (from clone DKFZp434B083)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-44
RA   Wambutt R., Heubner D., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by AGOWA within the cDNA
CC   sequencing consortium of the German Genome Project
CC   r1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .44
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434B083"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 44 BP; 6 A; 8 C; 3 G; 27 T; 0 other;


  Query Match             0.7%;  Score 17;  DB 2;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaaa 2566
           ||||||||||||||||||
Db      38 TGGAAAAAAAAAAAAAA 22


RESULT  10
HSM003634/c
ID   HSM003634  standard; RNA; EST; 45 BP.
XX
AC   AL039158;
XX
SV   AL039158.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566M244_s1  (from clone DKFZp566M244)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-45
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No r1 sequence available
CC   This clone is available at the RZPD in Berlin
```

```
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .45
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566M244"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 45 BP; 2 A; 10 C; 0 G; 33 T; 0 other;


  Query Match              0.7%;  Score 17;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     37 TGGAAAAAAAAAAAAAA 21


RESULT  11
BF017790
LOCUS       BF017790       49 bp    mRNA            EST       29-DEC-2000
DEFINITION  ux75h05.y1 McCarrey Eddy type B spermatogonia Mus musculus cDNA
            clone IMAGE:3654393 5', mRNA sequence.
ACCESSION   BF017790
VERSION     BF017790.1  GI:10749122
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1416697
            Seq primer: Primer name ambiguous.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3654393"
                     /clone_lib="McCarrey Eddy type B spermatogonia"
                     /sex="male"
                     /tissue_type="type B spermatogonia, pooled from multiple
                     mice"
                     /dev_stage="8 day"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: testis; Vector: pBluescript SK+ (Stratagene
                     ); Site_1: XhoI; Site_2: EcoRI; cDNA oligo dT-primed
                     [5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTT-3'] and directionally
                     cloned  using 5' linkers 5'-AATTCGGCACGAG-3' and
                     5'-CTCGTGCCG-3'. Size selection of >400bp material gives
                     average insert size ranging from 1-2 kb. Library was mass
                     excised (from  lambda-UniZAP-XR) and resulting
                     single-stranded phagemids were prepped and tranformed
                     into DH10B. Library contains 96% recombinants.
                     References: J. Androl. 20:635-639 and Gene 25:263-269.
                     Library constructed and donated by J. McCarrey, Ph.D.
                     (Southwest Foundation for Biomedical Research, Dept. of
                     Genetics); excision done by E.M. Eddy, Ph.D. (National
                     Institutes of  Health, National Institute of Environmental
                     Health Sciences).  Original lambda-based library is
                     available through ATCC, catalog #63417."
BASE COUNT       24 a      9 c      9 g      7 t
ORIGIN


  Query Match              0.7%;  Score 17;  DB 11;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     24 TGGAAAAAAAAAAAAAA 40


RESULT  12
HSM003660/c
ID   HSM003660  standard; RNA; EST; 50 BP.
XX
AC   AL039184;
XX
SV   AL039184.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566O064_s1  (from clone DKFZp566O064)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-50
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No r1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .50
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566O064"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 50 BP; 10 A; 10 C; 2 G; 28 T; 0 other;


  Query Match              0.7%;  Score 17;  DB 2;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+05;
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```
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      21 TGGAAAAAAAAAAAAA 5


RESULT  13
AZ853220
LOCUS       AZ853220       19 bp    DNA             GSS       21-FEB-2001
DEFINITION  2M0156J15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0156J15 F, DNA sequence.
ACCESSION   AZ853220
VERSION     AZ853220.1  GI:13041116
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0156  row: J  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0156J15"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       17 a      0 c      2 g      0 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       1 GGAAAAAAAAAAAAAA 16


RESULT  14
AZ856873/c
LOCUS       AZ856873       19 bp    DNA             GSS       21-FEB-2001
DEFINITION  2M0161O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0161O19 F, DNA sequence.
ACCESSION   AZ856873
VERSION     AZ856873.1  GI:13048296
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0161  row: O  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0161O19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      5 c      0 g     14 t
ORIGIN
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  Query Match             0.6%;  Score 16;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      16 GGAAAAAAAAAAAAAA 1


RESULT  15
AZ950028
LOCUS       AZ950028       19 bp    DNA             GSS       27-APR-2001
DEFINITION  2M0213L19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0213L19 R, DNA sequence.
ACCESSION   AZ950028
VERSION     AZ950028.1  GI:13821255
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0213  row: L  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0213L19"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       14 a      0 c      5 g      0 t
ORIGIN
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  Query Match             0.6%;  Score 16;  DB 13;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       4 GGAAAAAAAAAAAAAA 19


RESULT  16
AZ370699/c
LOCUS       AZ370699       20 bp    DNA             GSS       02-OCT-2000
DEFINITION  1M0121N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0121N17 R, DNA sequence.
ACCESSION   AZ370699
VERSION     AZ370699.1  GI:10484399
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0121  row: N  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0121N17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      2 c      0 g     18 t
ORIGIN
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  Query Match          0.6%;  Score 16;  DB 13;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     20 GGAAAAAAAAAAAAAA 5


RESULT  17
AZ406839
LOCUS       AZ406839       20 bp    DNA             GSS       03-OCT-2000
DEFINITION  1M0176C16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0176C16 F, DNA sequence.
ACCESSION   AZ406839
VERSION     AZ406839.1  GI:10530852
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0176  row: C  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0176C16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       8 a      7 c      2 g      3 t
ORIGIN


  Query Match          0.6%;  Score 16;  DB 13;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1768 cacacatacacacatg 1783
          ||||||||||||||||
Db      3 CACACATACACACATG 18


RESULT  18
AZ785791/c
LOCUS       AZ785791       21 bp    DNA             GSS       16-FEB-2001
DEFINITION  1M0030O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0030O19 F, DNA sequence.
ACCESSION   AZ785791
VERSION     AZ785791.1  GI:12922904
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0030  row: O  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0030O19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

```
BASE COUNT        0 a      7 c      0 g     14 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 13;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      16 GGAAAAAAAAAAAAAA 1


RESULT  19
HSM002940
ID   HSM002940  standard; RNA; EST; 22 BP.
XX
AC   AL038464;
XX
SV   AL038464.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566B0646_r1  (from clone DKFZp566B0646)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-22
RA   Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   s1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .22
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566B0646"
FT                   /clone_lib="566, (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 22 BP; 20 A; 0 C; 2 G; 0 T; 0 other;


  Query Match           0.6%;  Score 16;  DB 2;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       2 GGAAAAAAAAAAAAAA 17


RESULT  20
AZ309907/c
LOCUS       AZ309907       22 bp    DNA             GSS       29-SEP-2000
DEFINITION  1M0017N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0017N14 F, DNA sequence.
ACCESSION   AZ309907
VERSION     AZ309907.1  GI:10351367
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0017  row: N  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0017N14"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      3 c      0 g     19 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 13;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      21 GGAAAAAAAAAAAAAA 6


RESULT  21
TA386H07Q/c
LOCUS       TA386H07Q      22 bp    DNA             GSS       13-DEC-2000
```

```
DEFINITION  T. brucei sheared genomic DNA clone 386h07, reverse sequence,
            genomic survey sequence.
ACCESSION   AL498291
VERSION     AL498291.1  GI:11874013
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="386h07"
BASE COUNT        0 a      4 c      0 g     18 t
ORIGIN
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  Query Match             0.6%;  Score 16;  DB 13;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     20 GGAAAAAAAAAAAAAA 5


RESULT  22
AZ390689
LOCUS       AZ390689       23 bp    DNA             GSS       03-OCT-2000
DEFINITION  1M0152A18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0152A18 F, DNA sequence.
ACCESSION   AZ390689
VERSION     AZ390689.1  GI:10505732
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0152  row: A  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0152A18"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       16 a      0 c      7 g      0 t
ORIGIN
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  Query Match             0.6%;  Score 16;  DB 13;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      8 GGAAAAAAAAAAAAAA 23


RESULT  23
AZ812579
LOCUS       AZ812579       24 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0079A23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0079A23 F, DNA sequence.
ACCESSION   AZ812579
VERSION     AZ812579.1  GI:12981965
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
```

```
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0079  row: A  column: 23
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0079A23"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       22 a      0 c      2 g      0 t
ORIGIN


  Query Match              0.6%;  Score 16;  DB 13;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.7e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       1 GGAAAAAAAAAAAAAA 16


RESULT  24
HSM001398
ID   HSM001398  standard; RNA; EST; 25 BP.
XX
AC   AL037073;
XX
SV   AL037073.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564K1464_r1  (from clone DKFZp564K1464)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-25
RA   Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .25
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564K1464"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   X1-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 25 BP; 16 A; 0 C; 8 G; 1 T; 0 other;


  Query Match              0.6%;  Score 16;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       8 GGAAAAAAAAAAAAAA 23


RESULT  25
HSM003169/c
ID   HSM003169  standard; RNA; EST; 25 BP.
XX
AC   AL038693;
XX
SV   AL038693.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566J0846_s1  (from clone DKFZp566J0846)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-25
RA   Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   r1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .25
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566J0846"
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FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 25 BP; 1 A; 5 C; 0 G; 19 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     21 GGAAAAAAAAAAAAAA 6


RESULT  26
HSM003450
ID   HSM003450  standard; RNA; EST; 25 BP.
XX
AC   AL038974;
XX
SV   AL038974.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566A224_r1  (from clone DKFZp566A224)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-25
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .25
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566A224"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 25 BP; 18 A; 0 C; 7 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      6 GGAAAAAAAAAAAAAA 21


RESULT  27
AZ832800/c
LOCUS       AZ832800       25 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0113M21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0113M21 F, DNA sequence.
ACCESSION   AZ832800
VERSION     AZ832800.1  GI:13002708
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0113  row: M  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0113M21"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      2 c      0 g     23 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 13;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     25 GGAAAAAAAAAAAAAA 10
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RESULT  28
AZ837511/c
LOCUS       AZ837511        25 bp    DNA             GSS       20-FEB-2001
DEFINITION  2M0132N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0132N17 R, DNA sequence.
ACCESSION   AZ837511
VERSION     AZ837511.1  GI:13007419
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0132  row: N  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0132N17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        0 a      10 c       0 g      15 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 13;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     17 GGAAAAAAAAAAAAAA 2
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```
RESULT  29
TA324F07P/c
LOCUS       TA324F07P      25 bp    DNA             GSS       13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 324f07, forward sequence,
            genomic survey sequence.
ACCESSION   AL493403
VERSION     AL493403.1  GI:11867768
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="324f07"
BASE COUNT        0 a       9 c       0 g      16 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 13;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db     18 GGAAAAAAAAAAAAAA 3
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RESULT  30
HSM001401
ID   HSM001401  standard; RNA; EST; 26 BP.
XX
AC   AL037076;
XX
SV   AL037076.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564K1764_r1  (from clone DKFZp564K1764)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
```

```
RN   [1]
RP   1-26
RA   Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564K1764"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 26 BP; 18 A; 0 C; 8 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      7 GGAAAAAAAAAAAAAA 22


RESULT  31
HSM001421
ID   HSM001421  standard; RNA; EST; 26 BP.
XX
AC   AL037096;
XX
SV   AL037096.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564L2164_r1  (from clone DKFZp564L2164)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564L2164"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 26 BP; 21 A; 0 C; 5 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      4 GGAAAAAAAAAAAAAA 19


RESULT  32
HSM002179
ID   HSM002179  standard; RNA; EST; 26 BP.
XX
AC   AL037846;
XX
SV   AL037846.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564I177_r1  (from clone DKFZp564I177)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564I177"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 26 BP; 18 A; 0 C; 8 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
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Db      7 GGAAAAAAAAAAAAAA 22


RESULT  33
HSM002201/c
ID   HSM002201  standard; RNA; EST; 26 BP.
XX
AC   AL037868;
XX
SV   AL037868.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564J177_s1  (from clone DKFZp564J177)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   r1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564J177"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 26 BP; 0 A; 8 C; 0 G; 18 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     20 GGAAAAAAAAAAAAAA 5


RESULT  34
HSM003490
ID   HSM003490  standard; RNA; EST; 26 BP.
XX
AC   AL039014;
XX
SV   AL039014.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566C074_r1  (from clone DKFZp566C074)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566C074"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 26 BP; 18 A; 0 C; 8 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     7 GGAAAAAAAAAAAAAA 22


RESULT  35
HSM003529
ID   HSM003529  standard; RNA; EST; 26 BP.
XX
AC   AL039053;
XX
SV   AL039053.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566F044_r1  (from clone DKFZp566F044)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566F044"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 26 BP; 18 A; 0 C; 8 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      7 GGAAAAAAAAAAAAAA 22


RESULT  36
HSM003586
ID   HSM003586  standard; RNA; EST; 26 BP.
XX
AC   AL039110;
XX
SV   AL039110.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566J144_r1  (from clone DKFZp566J144)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-26
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .26
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566J144"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 26 BP; 19 A; 0 C; 7 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      6 GGAAAAAAAAAAAAAA 21


RESULT  37
HSM001542/c
ID   HSM001542  standard; RNA; EST; 27 BP.
XX
AC   AL037217;
XX
SV   AL037217.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564B0669_s1  (from clone DKFZp564B0669)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Ansorge W., Wirkner U., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by EMBL within the cDNA
CC   sequencing consortium of the German Genome Project
CC   r1 sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .27
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564B0669"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 27 BP; 0 A; 8 C; 0 G; 19 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db     21 GGAAAAAAAAAAAAAA 6


RESULT  38
HSM002015
ID   HSM002015  standard; RNA; EST; 27 BP.
XX
AC   AL037684;
XX
SV   AL037684.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
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DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564O1372_r1  (from clone DKFZp564O1372)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
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FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564O1372"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 27 BP; 19 A; 0 C; 8 G; 0 T; 0 other;


  Query Match              0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      7 GGAAAAAAAAAAAAAA 22


RESULT  39
HSM002125
ID   HSM002125  standard; RNA; EST; 27 BP.
XX
AC   AL037793;
XX
SV   AL037793.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564F137_r1  (from clone DKFZp564F137)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .27
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564F137"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 27 BP; 18 A; 0 C; 9 G; 0 T; 0 other;


  Query Match              0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
          ||||||||||||||||
Db      8 GGAAAAAAAAAAAAAA 23


RESULT  40
HSM002148/c
ID   HSM002148  standard; RNA; EST; 27 BP.
XX
AC   AL037815;
XX
SV   AL037815.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564G127_s1  (from clone DKFZp564G127)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No r1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .27
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FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564G127"
FT                   /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
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XX
SQ   Sequence 27 BP; 0 A; 9 C; 0 G; 18 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      20 GGAAAAAAAAAAAAAA 5


RESULT  41
HSM003588/c
ID   HSM003588  standard; RNA; EST; 27 BP.
XX
AC   AL039112;
XX
SV   AL039112.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566J184_s1  (from clone DKFZp566J184)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No r1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .27
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566J184"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 27 BP; 0 A; 8 C; 0 G; 19 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      21 GGAAAAAAAAAAAAAA 6


RESULT  42
HSM003597
ID   HSM003597  standard; RNA; EST; 27 BP.
XX
AC   AL039121;
XX
SV   AL039121.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp566J084_r1  (from clone DKFZp566J084)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-27
RA   Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .27
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FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp566J084"
FT                   /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT                   Xl-2blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 27 BP; 19 A; 0 C; 8 G; 0 T; 0 other;


  Query Match             0.6%;  Score 16;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       7 GGAAAAAAAAAAAAAA 22


RESULT  43
AV741507
LOCUS       AV741507       27 bp    mRNA            EST       17-OCT-2000
DEFINITION  AV741507 CB Homo sapiens cDNA clone CBMAMC05 5', mRNA sequence.
ACCESSION   AV741507
VERSION     AV741507.1  GI:10859088
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
```

```
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="CBMAMC05"
                      /clone_lib="CB"
                      /tissue_type="cord blood"
                      /cell_type="CD34+ hematopoietic stem/progenitor cell"
                      /lab_host="BM25.8"
                      /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                      cloned randomly with the EcoRI digestion"
BASE COUNT       17 a      2 c      6 g      0 t      2 others
ORIGIN


  Query Match              0.6%;  Score 16;  DB 10;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      11 GGAAAAAAAAAAAAAA 26


RESULT  44
N29432/c
LOCUS       N29432         27 bp    mRNA            EST       05-JAN-1996
DEFINITION  yw86h10.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:259171 3' similar to gb:X64559 TETRANECTIN PRECURSOR
            (HUMAN);; mRNA sequence.
ACCESSION   N29432
VERSION     N29432.1  GI:1147952
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: m13 -40 forward
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Homo sapiens"
                      /db_xref="GDB:3888877"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:259171"
                      /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                      /dev_stage="two placentae: one from 8 weeks and another
                      from 9 weeks post conception"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library constructed by Bento Soares and
                      M.Fatima Bonaldo."
BASE COUNT       0 a      3 c      0 g     24 t
ORIGIN


  Query Match              0.6%;  Score 16;  DB 11;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      25 GGAAAAAAAAAAAAAA 10


RESULT  45
R31539/c
LOCUS       R31539         27 bp    mRNA            EST       28-APR-1995
DEFINITION  yh72e05.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
            IMAGE:135296 3' similar to gb:X53463 GLUTATHIONE
            PEROXIDASE-GASTROINTESTINAL (HUMAN);; mRNA sequence.
ACCESSION   R31539
VERSION     R31539.1  GI:787382
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 367
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 367   Std Error: 0.00
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Homo sapiens"
                      /db_xref="GDB:541217"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:135296"
                      /clone_lib="Soares placenta Nb2HP"
                      /sex="Female"
                      /dev_stage="placenta obtained at birth (full term)"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
```

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT 0 a 2 c 0 g 24 t 1 others
ORIGIN

Query Match 0.6%; Score 16; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 9e+05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      27 GGAAAAAAAAAAAAAA 12
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Search completed: April 20, 2002, 09:07:17
Job time: 8699 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 20, 2002, 06:44:33 ; Search time 3629.2 Seconds
(without alignments)
11664.213 Million cell updates/sec

Title: US-10-024-396-3
Perfect score: 2566
Sequence: 1 cgtcgccgtccccgtctcct.....aaatggaaaaaaaaaaaaaa 2566

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		31	1.2	34	6	AR112204	AR112204 Sequence
2		31	1.2	34	6	AR149246	AR149246 Sequence
3	c	26	1.0	33	6	AR096476	AR096476 Sequence
4	c	24	0.9	24	6	AR092018	AR092018 Sequence
5	c	24	0.9	24	6	AR112153	AR112153 Sequence
6	c	24	0.9	24	6	AR149195	AR149195 Sequence
7	c	23	0.9	23	6	AR112201	AR112201 Sequence
8	c	23	0.9	23	6	AR149243	AR149243 Sequence
9	c	23	0.9	31	6	AR092048	AR092048 Sequence
10		23	0.9	31	6	AR092050	AR092050 Sequence
11	c	23	0.9	31	6	AR112183	AR112183 Sequence
12		23	0.9	31	6	AR112185	AR112185 Sequence
13	c	23	0.9	31	6	AR149225	AR149225 Sequence
14		23	0.9	31	6	AR149227	AR149227 Sequence
15		18	0.7	36	6	AR096475	AR096475 Sequence
16	c	18	0.7	50	6	AX161232	AX161232 Sequence
17	c	17	0.7	20	6	AR092047	AR092047 Sequence
18		17	0.7	20	6	AR092049	AR092049 Sequence
19	c	17	0.7	20	6	AR112182	AR112182 Sequence
20		17	0.7	20	6	AR112184	AR112184 Sequence
21	c	17	0.7	20	6	AR149224	AR149224 Sequence
22		17	0.7	20	6	AR149226	AR149226 Sequence
23	c	17	0.7	25	6	AX043026	AX043026 Sequence
24	c	17	0.7	47	6	AR142905	AR142905 Sequence
25	c	16	0.6	18	6	E32461	E32461 Mammal-deri
26	c	16	0.6	20	6	E29883	E29883 HIV cofacto
27	c	16	0.6	22	6	AR142908	AR142908 Sequence
28		16	0.6	23	6	AX115478	AX115478 Sequence
29		16	0.6	25	6	A90999	A90999 Sequence 1
30		16	0.6	25	6	A91901	A91901 Sequence 5
31		16	0.6	25	6	AR106367	AR106367 Sequence
32		16	0.6	25	6	AR148371	AR148371 Sequence
33		16	0.6	25	6	AX032404	AX032404 Sequence
34	c	16	0.6	25	6	AX042532	AX042532 Sequence
35	c	16	0.6	25	6	AX042542	AX042542 Sequence
36	c	16	0.6	25	6	AX042571	AX042571 Sequence
37	c	16	0.6	25	6	AX042589	AX042589 Sequence
38	c	16	0.6	25	6	AX042627	AX042627 Sequence
39	c	16	0.6	25	6	AX042759	AX042759 Sequence
40	c	16	0.6	25	6	AX042823	AX042823 Sequence
41	c	16	0.6	25	6	AX042825	AX042825 Sequence
42	c	16	0.6	25	6	AX042827	AX042827 Sequence
43	c	16	0.6	25	6	AX042871	AX042871 Sequence
44	c	16	0.6	25	6	AX042878	AX042878 Sequence
45		16	0.6	25	13	AX032410	AX032410 Sequence

ALIGNMENTS

RESULT 1
AR112204
LOCUS AR112204 34 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 93 from patent US 6130041.
ACCESSION AR112204
VERSION AR112204.1 GI:14092104
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Acton,S.Laurene.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 93 10-OCT-2000;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
BASE COUNT 4 a 15 c 3 g 12 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.1e-05;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1085 ccttgtttctctcccatcctcacttcctcaa 1115
          ||||||||||||||||||||||||||||||
Db      1 CCTTGTTTCTCTCCCATCCTCACTTCCTCAA 31


RESULT   2
AR149246
LOCUS       AR149246       34 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 93 from patent US 6228581.
ACCESSION   AR149246
VERSION     AR149246.1  GI:15113837
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6228581-A 93 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
BASE COUNT        4 a      15 c       3 g      12 t
ORIGIN


  Query Match             1.2%;  Score 31;  DB 6;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-05;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1085 ccttgtttctctcccatcctcacttcctcaa 1115
          ||||||||||||||||||||||||||||||
Db      1 CCTTGTTTCTCTCCCATCCTCACTTCCTCAA 31


RESULT   3
AR096476/c
LOCUS       AR096476       33 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 5 from patent US 6008014.
ACCESSION   AR096476
VERSION     AR096476.1  GI:10025312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Gimeno,C.J. and Acton,S.
  TITLE     Method of making lipid metabolic pathway compositions
  JOURNAL   Patent: US 6008014-A 5 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        6 a      10 c       7 g      10 t
ORIGIN


  Query Match             1.0%;  Score 26;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1576 gtgctgcaggaagcaaaactgtaggg 1601
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Db     33 GTGCTGCAGGAAGCAAAACTGTAGGG 8


RESULT   4
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AR092018/c
LOCUS       AR092018       24 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 42 from patent US 5998141.
ACCESSION   AR092018
VERSION     AR092018.1  GI:10018772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Acton,S.Laurene.
  TITLE     Intronic and polymorphic SR-BI nucleic acids and uses therefor
  JOURNAL   Patent: US 5998141-A 42 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        3 a      8 c      8 g      5 t
ORIGIN


  Query Match             0.9%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     67 gacatgggctgctccgccaaagcg 90
          ||||||||||||||||||||||||
Db     24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   5
AR112153/c
LOCUS       AR112153       24 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 42 from patent US 6130041.
ACCESSION   AR112153
VERSION     AR112153.1  GI:14092053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6130041-A 42 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        3 a      8 c      8 g      5 t
ORIGIN


  Query Match             0.9%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     67 gacatgggctgctccgccaaagcg 90
          ||||||||||||||||||||||||
Db     24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   6
AR149195/c
LOCUS       AR149195       24 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 42 from patent US 6228581.
ACCESSION   AR149195
VERSION     AR149195.1  GI:15113786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
```

```
          therefor
  JOURNAL   Patent: US 6228581-A 42 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        3 a      8 c      8 g      5 t
ORIGIN

  Query Match             0.9%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 gacatgggctgctccgccaaagcg 90
           ||||||||||||||||||||||||
Db      24 GACATGGGCTGCTCCGCCAAAGCG 1


RESULT   7
AR112201/c
LOCUS       AR112201        23 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 90 from patent US 6130041.
ACCESSION   AR112201
VERSION     AR112201.1  GI:14092101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6130041-A 90 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        6 a      10 c      6 g      1 t
ORIGIN

  Query Match             0.9%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     123 gctactgtgcgctgtgctgggcg 145
           |||||||||||||||||||||||
Db      23 GCTACTGTGCGCTGTGCTGGGCG 1


RESULT   8
AR149243/c
LOCUS       AR149243        23 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 90 from patent US 6228581.
ACCESSION   AR149243
VERSION     AR149243.1  GI:15113834
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6228581-A 90 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        6 a      10 c      6 g      1 t
ORIGIN

  Query Match             0.9%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     123 gctactgtgcgctgtgctgggcg 145
           |||||||||||||||||||||||
Db      23 GCTACTGTGCGCTGTGCTGGGCG 1


RESULT   9
AR092048/c
LOCUS       AR092048        31 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 72 from patent US 5998141.
ACCESSION   AR092048
VERSION     AR092048.1  GI:10018802
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.Laurene.
  TITLE     Intronic and polymorphic SR-BI nucleic acids and uses therefor
  JOURNAL   Patent: US 5998141-A 72 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        7 a      6 c      12 g      6 t
ORIGIN

  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggttctggca 1134
           ||||||||||||||||||||||
Db      23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  10
AR092050
LOCUS       AR092050        31 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 74 from patent US 5998141.
ACCESSION   AR092050
VERSION     AR092050.1  GI:10018804
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.Laurene.
  TITLE     Intronic and polymorphic SR-BI nucleic acids and uses therefor
  JOURNAL   Patent: US 5998141-A 74 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        6 a      12 c      6 g      7 t
ORIGIN

  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1112 tcaacgccgacccggttctggca 1134
           ||||||||||||||||||||||
Db       9 TCAACGCCGACCCGGTTCTGGCA 31


RESULT  11
AR112183/c
LOCUS       AR112183        31 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 72 from patent US 6130041.
ACCESSION   AR112183
VERSION     AR112183.1  GI:14092083
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6130041-A 72 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        7 a      6 c     12 g      6 t
ORIGIN


  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db     23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  12
AR112185
LOCUS       AR112185       31 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 74 from patent US 6130041.
ACCESSION   AR112185
VERSION     AR112185.1  GI:14092085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6130041-A 74 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        6 a      12 c      6 g      7 t
ORIGIN


  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      9 TCAACGCCGACCCGGTTCTGGCA 31


RESULT  13
AR149225/c
LOCUS       AR149225       31 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 72 from patent US 6228581.
ACCESSION   AR149225
VERSION     AR149225.1  GI:15113816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6228581-A 72 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        7 a      6 c     12 g      6 t
ORIGIN


  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db     23 TCAACGCCGACCCGGTTCTGGCA 1


RESULT  14
AR149227
LOCUS       AR149227       31 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 74 from patent US 6228581.
ACCESSION   AR149227
VERSION     AR149227.1  GI:15113818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6228581-A 74 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="unknown"
BASE COUNT        6 a      12 c      6 g      7 t
ORIGIN


  Query Match             0.9%;  Score 23;  DB 6;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggttctggca 1134
           |||||||||||||||||||||||
Db      9 TCAACGCCGACCCGGTTCTGGCA 31


RESULT  15
AR096475
LOCUS       AR096475       36 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 4 from patent US 6008014.
ACCESSION   AR096475
VERSION     AR096475.1  GI:10025310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Gimeno,C.J. and Acton,S.
  TITLE     Method of making lipid metabolic pathway compositions
  JOURNAL   Patent: US 6008014-A 4 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="unknown"
BASE COUNT       10 a      9 c     10 g      7 t
ORIGIN


  Query Match             0.7%;  Score 18;  DB 6;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1456 caaatccggagccaagag 1473
           ||||||||||||||||||
Db     19 CAAATCCGGAGCCAAGAG 36
```

```
RESULT  16
AX161232/c
LOCUS       AX161232       50 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 4560 from Patent WO0140521.
ACCESSION   AX161232
VERSION     AX161232.1  GI:14542563
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 4560 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg43958770"
     misc_feature    26
                     /note="2 of 2 allelic variants (4559 is other entry)"
BASE COUNT       16 a      4 c      5 g     25 t
ORIGIN


  Query Match             0.7%;  Score 18;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2544 aaaaaatggaaaaaaaaa 2561
           ||||||||||||||||||
Db     43 AAAAAATGGAAAAAAAAA 26


RESULT  17
AR092047/c
LOCUS       AR092047       20 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 71 from patent US 5998141.
ACCESSION   AR092047
VERSION     AR092047.1  GI:10018801
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.Laurene.
  TITLE     Intronic and polymorphic SR-BI nucleic acids and uses therefor
  JOURNAL   Patent: US 5998141-A 71 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      8 g      4 t
ORIGIN


  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db     17 TCAACGCCGACCCGGTT 1


RESULT  18
AR092049
LOCUS       AR092049       20 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 73 from patent US 5998141.
ACCESSION   AR092049
VERSION     AR092049.1  GI:10018803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.Laurene.
  TITLE     Intronic and polymorphic SR-BI nucleic acids and uses therefor
  JOURNAL   Patent: US 5998141-A 73 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      8 c      4 g      4 t
ORIGIN


  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db      4 TCAACGCCGACCCGGTT 20


RESULT  19
AR112182/c
LOCUS       AR112182       20 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 71 from patent US 6130041.
ACCESSION   AR112182
VERSION     AR112182.1  GI:14092082
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6130041-A 71 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      8 g      4 t
ORIGIN


  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
           |||||||||||||||||
Db     17 TCAACGCCGACCCGGTT 1


RESULT  20
AR112184
LOCUS       AR112184       20 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 73 from patent US 6130041.
ACCESSION   AR112184
VERSION     AR112184.1  GI:14092084
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.Laurene.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
```

```
  JOURNAL   Patent: US 6130041-A 73 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      8 c      4 g      4 t
ORIGIN

  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
        |||||||||||||||||
Db      4 TCAACGCCGACCCGGTT 20


RESULT  21
AR149224/c
LOCUS       AR149224        20 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 71 from patent US 6228581.
ACCESSION   AR149224
VERSION     AR149224.1  GI:15113815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses.
            therefor
  JOURNAL   Patent: US 6228581-A 71 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      8 g      4 t
ORIGIN

  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
        |||||||||||||||||
Db     17 TCAACGCCGACCCGGTT 1


RESULT  22
AR149226
LOCUS       AR149226        20 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 73 from patent US 6228581.
ACCESSION   AR149226
VERSION     AR149226.1  GI:15113817
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Acton,S.L. and Ordovas,J.M.
  TITLE     Human intronic and polymorphic SR-BI nucleic acids and uses
            therefor
  JOURNAL   Patent: US 6228581-A 73 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      8 c      4 g      4 t
ORIGIN

  Query Match             0.7%;  Score 17;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1112 tcaacgccgacccggtt 1128
        |||||||||||||||||
Db      4 TCAACGCCGACCCGGTT 20


RESULT  23
AX043026/c
LOCUS       AX043026        25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 592 from Patent WO0065088.
ACCESSION   AX043026
VERSION     AX043026.1  GI:11341634
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 592 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE).
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"
BASE COUNT        2 a      3 c      3 g     17 t
ORIGIN

  Query Match             0.7%;  Score 17;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2549 atggaaaaaaaaaaaaa 2565
        |||||||||||||||||
Db     17 ATGGAAAAAAAAAAAAA 1


RESULT  24
AR142905/c
LOCUS       AR142905        47 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 1 from patent US 6204024.
ACCESSION   AR142905
VERSION     AR142905.1  GI:15104191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Romano,J.W. and Lee,E.Mi.
  TITLE     CCR5 RNA transcription based amplification assay
  JOURNAL   Patent: US 6204024-A 1 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       15 a     14 c     11 g      7 t
ORIGIN

  Query Match             0.7%;  Score 17;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgctc 1311
        |||||||||||||||||
Db     41 TGGTCCTGCCGCTGCTC 25


RESULT  25
E32461/c
LOCUS       E32461          18 bp    DNA             PAT       07-FEB-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
```

```
ACCESSION   E32461
VERSION     E32461.1  GI:13018697
KEYWORDS    JP 2000037190-A/21.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N.Y.N.N. and Tanaka.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 21 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/21
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
           C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT        0 a       2 c       1 g      15 t
ORIGIN
```

```
  Query Match             0.6%;  Score 16;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      18 GGAAAAAAAAAAAAAA 3
```

```
RESULT  26
E29883/c
LOCUS       E29883          20 bp    DNA             PAT       07-FEB-2001
DEFINITION  HIV cofactor inhibitor.
ACCESSION   E29883
VERSION     E29883.1  GI:13021278
KEYWORDS    JP 1999292795-A/37.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hiroshi,T.N.Y.Y. and Kimura,K.T.A.A.
  TITLE     HIV cofactor inhibitor
  JOURNAL   Patent: JP 1999292795-A 37 26-OCT-1999;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999292795-A/37
            PD   26-OCT-1999
            PF   02-APR-1998 JP 1998125452
            PR
            PI   HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
              AKIRA WADA
            PC   A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /db_xref="taxon:32644"
BASE COUNT        5 a       8 c       7 g       0 t
ORIGIN
```

```
  Query Match             0.6%;  Score 16;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1295 tggtcctgccgctgct 1310
           ||||||||||||||||
Db      16 TGGTCCTGCCGCTGCT 1
```

```
RESULT  27
AR142908/c
LOCUS       AR142908        22 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 4 from patent US 6204024.
ACCESSION   AR142908
VERSION     AR142908.1  GI:15104194
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Romano,J.W. and Lee,E.Mi.
  TITLE     CCR5 RNA transcription based amplification assay
  JOURNAL   Patent: US 6204024-A 4 20-MAR-2001;
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unknown"
BASE COUNT        6 a       9 c       7 g       0 t
ORIGIN
```

```
  Query Match             0.6%;  Score 16;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1295 tggtcctgccgctgct 1310
           ||||||||||||||||
Db      16 TGGTCCTGCCGCTGCT 1
```

```
RESULT  28
AX115478
LOCUS       AX115478        23 bp    DNA             PAT       11-MAY-2001
DEFINITION  Sequence 601 from Patent WO0129262.
ACCESSION   AX115478
VERSION     AX115478.1  GI:14032420
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct .
            artificial sequence.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 601 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
                      /note="Primer"
BASE COUNT       16 a       1 c       5 g       1 t
ORIGIN
```

```
  Query Match             0.6%;  Score 16;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db       5 GGAAAAAAAAAAAAAA 20
```

```
RESULT 29
A90999
LOCUS       A90999         25 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 1 from Patent EP0854196.
ACCESSION   A90999
VERSION     A90999.1  GI:6739605
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Paeaebo,S.E. and Kilger,C.A.
  TITLE     Method for the uncoupled, direct, exponential amplification and
            sequencing of DNA molecules with the addition of a second
            thermostable DNA polymerase and its application
  JOURNAL   Patent: EP 0854196-A 1 22-JUL-1998;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT 30
A91901
LOCUS       A91901         25 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 5 from Patent EP0849364.
ACCESSION   A91901
VERSION     A91901.1  GI:6740774
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Paeaebo,S.E. and Kilger,C.A.
  TITLE     Method for the direct, exponential amplification and sequencing of
            DNA molecules and its application
  JOURNAL   Patent: EP 0849364-A 5 24-JUN-1998;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT 31
AR106367
LOCUS       AR106367       25 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 5 from patent US 6107032.
ACCESSION   AR106367
VERSION     AR106367.1  GI:12820897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kilger,C. and Paabo,S.
  TITLE     Method for the direct, exponential amplification and sequencing of
            DNA molecules and its application
  JOURNAL   Patent: US 6107032-A 5 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT 32
AR148371
LOCUS       AR148371       25 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 1 from patent US 6225092.
ACCESSION   AR148371
VERSION     AR148371.1  GI:15112461
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kilger,C. and Paabo,S.
  TITLE     Method for the uncoupled, direct, exponential amplification and
            sequence of DNA molecules with the addition of a second
            thermostable DNA polymerase and its application
  JOURNAL   Patent: US 6225092-A 1 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match           0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT 33
AX032404
LOCUS       AX032404       25 bp    DNA             PAT       20-SEP-2000
DEFINITION  Sequence 5 from Patent EP1004677.
ACCESSION   AX032404
VERSION     AX032404.1  GI:10279377
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Paeaebo,S.E. and Kilger,C.A.
  TITLE     Method for the direct, exponential amplification and
  JOURNAL   Patent: EP 1004677-A 5 31-MAY-2000;
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            ROCHE DIAGNOSTICS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


RESULT  34
AX042532/c
LOCUS       AX042532       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 98 from Patent WO0065088.
ACCESSION   AX042532
VERSION     AX042532.1  GI:11341140
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 98 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"
BASE COUNT        2 a      6 c      1 g     16 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  35
AX042542/c
LOCUS       AX042542       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 108 from Patent WO0065088.
ACCESSION   AX042542
VERSION     AX042542.1  GI:11341150
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 108 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"
BASE COUNT        5 a      3 c      2 g     15 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  36
AX042571/c
LOCUS       AX042571       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 137 from Patent WO0065088.
ACCESSION   AX042571
VERSION     AX042571.1  GI:11341179
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 137 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"
BASE COUNT        2 a      6 c      2 g     15 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  37
AX042589/c
LOCUS       AX042589       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 155 from Patent WO0065088.
ACCESSION   AX042589
VERSION     AX042589.1  GI:11341197
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 155 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"
BASE COUNT        0 a      6 c      1 g     18 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2551 ggaaaaaaaaaaaaaa 2566
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              ||||||||||||||||
Db      16 GGAAAAAAAAAAAAAA 1


RESULT  38
AX042627/c
LOCUS       AX042627          25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 193 from Patent WO0065088.
ACCESSION   AX042627
VERSION     AX042627.1  GI:11341235
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 193 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="DRB1 Homozygote Primer Sequence"
BASE COUNT        2 a      5 c      4 g     14 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaa 2565
           ||||||||||||||||
Db      16 TGGAAAAAAAAAAAAA 1


RESULT  39
AX042759/c
LOCUS       AX042759          25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 325 from Patent WO0065088.
ACCESSION   AX042759
VERSION     AX042759.1  GI:11341367
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 325 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"
BASE COUNT        3 a      2 c      4 g     16 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2550 tggaaaaaaaaaaaaa 2565
           ||||||||||||||||
Db      16 TGGAAAAAAAAAAAAA 1


RESULT  40
AX042823/c
LOCUS       AX042823          25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 389 from Patent WO0065088.
ACCESSION   AX042823
VERSION     AX042823.1  GI:11341431
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 389 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"
BASE COUNT        3 a      7 c      0 g     15 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      16 GGAAAAAAAAAAAAAA 1


RESULT  41
AX042825/c
LOCUS       AX042825          25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 391 from Patent WO0065088.
ACCESSION   AX042825
VERSION     AX042825.1  GI:11341433
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 391 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"
BASE COUNT        2 a      7 c      1 g     15 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2551 ggaaaaaaaaaaaaaa 2566
           ||||||||||||||||
Db      16 GGAAAAAAAAAAAAAA 1


RESULT  42
AX042827/c
LOCUS       AX042827          25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 393 from Patent WO0065088.
ACCESSION   AX042827
VERSION     AX042827.1  GI:11341435
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
```

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REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 393 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"
BASE COUNT        2 a      7 c      2 g     14 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  43
AX042871/c
LOCUS       AX042871       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 437 from Patent WO0065088.
ACCESSION   AX042871
VERSION     AX042871.1  GI:11341479
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 437 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-C Homozygote Primer Sequence"
BASE COUNT        5 a      2 c      2 g     16 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  44
AX042878/c
LOCUS       AX042878       25 bp    DNA             PAT       23-NOV-2000
DEFINITION  Sequence 444 from Patent WO0065088.
ACCESSION   AX042878
VERSION     AX042878.1  GI:11341486
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 444 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="HLA-C Homozygote Primer Sequence"
BASE COUNT        3 a      2 c      4 g     16 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2550 tggaaaaaaaaaaaaa 2565
          ||||||||||||||||
Db     16 TGGAAAAAAAAAAAAA 1


RESULT  45
AX032410
LOCUS       AX032410       25 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 5 from Patent EP1004677.
ACCESSION   AX032410
VERSION     AX032410.1  GI:10279383
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Paeaebo,S.E. and Kilger,C.A.
  TITLE     Method for the direct, exponential amplification and
  JOURNAL   Patent: EP 1004677-A 31-MAY-2000;
            ROCHE DIAGNOSTICS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      8 c      8 g      8 t
ORIGIN


  Query Match             0.6%;  Score 16;  DB 13;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1295 tggtcctgccgctgct 1310
          ||||||||||||||||
Db      4 TGGTCCTGCCGCTGCT 19


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